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OM protein - protein search, using sw model

Run on: July 4, 2004, 07:21:48 ; Search time 76 Seconds
(without alignments)
1197.109 Million cell updates/sec

Title: US-09-787-879c-1
Perfect score: 1688
Sequence: 1 MDSIPVLGTELTPIINGREE.....EGGWLQFETLELSGRLEQ 322

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04: *
1: Geneseqp1980s: *
2: Geneseqp1990s: *
3: Geneseqp2000s: *
4: Geneseqp2001s: *
5: Geneseqp2002s: *
6: Geneseqp2003as: *
7: Geneseqp2003bs: *
8: Geneseqp2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query % Match	Length	DB ID	Description
1	1688	100.0	322	3	Aay90761 Human G p
2	1688	100.0	322	5	Abj04077 Human G p
3	1688	100.0	322	5	Aae21296 Human Mrg
4	1688	100.0	322	6	Abp81750 Human G p
5	1688	100.0	337	5	Aau97598 Human G-p
6	1683	99.7	322	3	Aay90762 Human G p
7	1683	99.7	322	7	Adc86821 Human GPC
8	1663	98.5	322	3	Aab14846 Human nov
9	1642	97.3	322	2	Aay30159 Human dor
10	1598	94.7	322	2	Aay30160 Human dor
11	1557	92.2	302	6	Abp96695 Human G p
12	1405	83.2	322	2	Aay30161 Human dor
13	1399	82.9	304	7	Adc12766 Human GPC
14	1391	82.4	322	2	Aay30162 Human dor
15	1387	82.2	322	3	Aay97664 Human G p
16	1387	82.2	322	7	Adc17728 Human TGR
17	1383	81.9	322	4	Aag54294 Human GTP
18	1383	81.9	322	4	Aae12794 Human G p
19	1383	81.9	322	4	Aau04371 Human G-p
20	1383	81.9	322	5	Aae17074 Human G-p
21	1383	81.9	322	5	Abp95617 Human GPC
22	1383	81.9	322	5	Aae21288 Human Mrg
23	1383	81.9	322	6	Abp96696 Human G p
24	1383	81.9	322	6	Abp95266 Human Dor
25	1383	81.9	322	7	Adc86445 Human GPC

26	1383	81.9	322	7	ABW00803	Abw00803 Human GPC
27	1379	81.7	322	2	Aay30163	Aay30163 Human dor
28	1367	81.0	322	3	Aay87663	Aay87663 Human G p
29	1367	81.0	322	5	ABJ04076	Abj04076 Human G p
30	1367	81.0	322	5	AAE21297	Aae21297 Human Mrg
31	1367	81.0	322	6	ABP96692	Abp96692 Human G p
32	1367	81.0	322	6	ABP81758	Abp81758 Human Mrg
33	1367	81.0	322	7	ADC17723	Adc17723 Human TGR
34	1361	80.6	322	7	ADC86589	Adc86589 Human GPC
35	1360	80.6	322	2	Aay30164	Aay30164 Human dor
36	1263	74.8	328	7	ADD18024	Add18024 Human G-p
37	1198	71.0	304	7	ADC12762	Adc12762 Human GPC
38	1031.5	61.1	331	5	ABP79885	Abp79885 Amino aci
39	989.5	58.6	330	4	AAG62852	Aag62852 Amino aci
40	989.5	58.6	330	4	AAG54301	Aag54301 Human GTP
41	989.5	58.6	330	4	AAY72910	Aay72910 Human IGS
42	989.5	58.6	330	4	AAB57654	Aab57654 Amino aci
43	989.5	58.6	330	4	AAU04376	Aau04376 Human G-p
44	989.5	58.6	330	5	AAE15639	Aae15639 Human G-p
45	989.5	58.6	330	5	ABB06258	Abb06258 Human G p

ALIGNMENTS

RESULT 1
AAY90761
ID AAY90761 standard; protein; 322 AA.
XX
AC AAY90761;
XX
DT 18-AUG-2000 (first entry)
XX
DE Human G protein-coupled receptor hH17213 SEQ ID NO:1.
XX
KW Human; G protein-coupled receptor; hippocampus; diagnosis; screening;
KW genetic disease; cellular function regulation.
XX
OS Homo sapiens.
XX
PN WO200020455-A1.
XX
PD 13-APR-2000.
XX
PF 30-SEP-1999; 99WO-JP005366.
XX
PR 01-OCT-1998; 98JP-00279535.
XX
(TAKE) TAKEDA CHEM IND LTD.
XX
PI Watanabe T, Terao Y, Matsui H;
XX
DR WPI; 2000-303747/26.
XX
N-PSDB; AAA29811.
XX
Human-derived G protein-coupled protein and encoding nucleic acid, useful
e.g. in determining ligands and treatment of diseases associated with
dysfunction of the protein.
XX
Claim 1; Page 90-91; 97pp; Japanese.

The present sequence represents a human-derived G protein-coupled protein designated hH17213, which is isolated from the human hippocampus. The G protein-coupled receptor can be used for preventing, treating and diagnosing genetic diseases associated with G protein-coupled protein, and for regulating cellular functions. The protein can be used to prevent and treat disorders associated with G protein-coupled protein gene dysfunction. It can also be used to identify G protein-coupled protein ligands and generating antibodies and antisera against the protein. It is also useful in constructing recombinant receptor protein expression systems, developing receptor-binding assay systems and screening drug candidates, and can be used as a probe in the genetic diagnosis of G protein-coupled protein disorders

```
XX SQ Sequence 322 AA;
Query Match 100.0%; Score 1688; DB 3; Length 322;
Best Local Similarity 100.0%; Pred. No. 2e-174;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDSTIPVLGTELTPIINGREETPCYKQTLSTGLTCTIVSLVALTGNVAVLWLLGCRMRNA 60
DB 1 MDSTIPVLGTELTPIINGREETPCYKQTLSTGLTCTIVSLVALTGNVAVLWLLGCRMRNA 60
QY 61 VSIYILNLVAADFLFLSGHIIICSPRLINIRHPISKILSPVMTFPFYFGLSMLSAISTER 120
DB 61 VSIYILNLVAADFLFLSGHIIICSPRLINIRHPISKILSPVMTFPFYFGLSMLSAISTER 120
QY 121 CLSILPMTWYHCRPRYLSSVMCVLLWALSILSLRSILEWMFCDFLFGSADSVMCETSDFTT 180
DB 121 CLSILPMTWYHCRPRYLSSVMCVLLWALSILSLRSILEWMFCDFLFGSADSVMCETSDFTT 180
QY 181 IAWLVFLCVLCCGSSLLVRLICGSRKMPLETLTYVITLLTVLVLFCGLPFGIQWALFS 240
DB 181 IAWLVFLCVLCCGSSLLVRLICGSRKMPLETLTYVITLLTVLVLFCGLPFGIQWALFS 240
QY 241 RIHLWKVLFCHVHLVSIPLSALNSSANPIIYFFVGSFRQRQNRQNLKVLQALQDTPE 300
DB 241 RIHLWKVLFCHVHLVSIPLSALNSSANPIIYFFVGSFRQRQNRQNLKVLQALQDTPE 300
QY 301 VDEGGWLPQETLELSGRLEQ 322
DB 301 VDEGGWLPQETLELSGRLEQ 322
RESULT 2
ABJ04077
ID ABJ04077 standard; protein; 322 AA.
XX AC ABJ04077;
XX DT 11-OCT-2002 (first entry)
XX DE Human G protein coupled receptor hRUP37.
XX KW Human; G-protein coupled receptor; GPCR; hRUP28; hRUP29; hRUP30; hRUP31;
XX KW hRUP32; hRUP33; hRUP34; hRUP35; hRUP36; hRUP37.
XX OS Homo sapiens.
XX PN WO200242461-A2.
XX PD 30-MAY-2002.
XX PF 26-NOV-2001; 2001WO-US044386.
XX PR 27-NOV-2000; 2000US-0253404P.
XX PR 12-DEC-2000; 2000US-0255366P.
XX PR 20-FEB-2001; 2001US-0270286P.
XX PR 20-FEB-2001; 2001US-0270286P.
XX PR 06-APR-2001; 2001US-0282032P.
XX PR 06-APR-2001; 2001US-0282356P.
XX PR 06-APR-2001; 2001US-0282356P.
XX PR 06-APR-2001; 2001US-0282356P.
XX PR 14-MAY-2001; 2001US-0290917P.
XX PR 31-JUL-2001; 2001US-0309208P.
XX PA (AREN-) ARENA PHARM INC.
XX PI Chen R, Chu ZL, Dang HT, Lowitz KP, Pride C;
XX WPI; 2002-566565/60.
XX N-PSDB; ABT04875.
XX Novel endogenous and non-endogenous versions of G protein-coupled
PT receptor useful for identification of candidate compounds as receptor
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PT agonists or antagonists for use as therapeutic agents.
XX Claim 37; Page 75-76; 84pp; English.
XX The present invention provides the protein and coding sequences of
XX several human G-protein coupled receptors (GPCRs). These can be used in
XX the identification of candidate compounds as receptor agonists or inverse
XX agonists having applicability as therapeutic agents. The present sequence
XX is a GPCR protein of the invention
XX Sequence 322 AA;
Query Match 100.0%; Score 1688; DB 5; Length 322;
Best Local Similarity 100.0%; Pred. No. 2e-174;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDSTIPVLGTELTPIINGREETPCYKQTLSTGLTCTIVSLVALTGNVAVLWLLGCRMRNA 60
DB 1 MDSTIPVLGTELTPIINGREETPCYKQTLSTGLTCTIVSLVALTGNVAVLWLLGCRMRNA 60
QY 61 VSIYILNLVAADFLFLSGHIIICSPRLINIRHPISKILSPVMTFPFYFGLSMLSAISTER 120
DB 61 VSIYILNLVAADFLFLSGHIIICSPRLINIRHPISKILSPVMTFPFYFGLSMLSAISTER 120
QY 121 CLSILPMTWYHCRPRYLSSVMCVLLWALSILSLRSILEWMFCDFLFGSADSVMCETSDFTT 180
DB 121 CLSILPMTWYHCRPRYLSSVMCVLLWALSILSLRSILEWMFCDFLFGSADSVMCETSDFTT 180
QY 181 IAWLVFLCVLCCGSSLLVRLICGSRKMPLETLTYVITLLTVLVLFCGLPFGIQWALFS 240
DB 181 IAWLVFLCVLCCGSSLLVRLICGSRKMPLETLTYVITLLTVLVLFCGLPFGIQWALFS 240
QY 241 RIHLWKVLFCHVHLVSIPLSALNSSANPIIYFFVGSFRQRQNRQNLKVLQALQDTPE 300
DB 241 RIHLWKVLFCHVHLVSIPLSALNSSANPIIYFFVGSFRQRQNRQNLKVLQALQDTPE 300
QY 301 VDEGGWLPQETLELSGRLEQ 322
DB 301 VDEGGWLPQETLELSGRLEQ 322
RESULT 3
AAE21296
ID AAE21296 standard; protein; 322 AA.
XX AC AAE21296;
XX DT 01-JUL-2002 (first entry)
XX DE Human MrgX3 (mas-related gene) protein.
XX KW Human; mas-related gene; G-protein coupled receptor; drg-12 protein;
XX KW receptor; sensory perception; pain; analgesic; MrgX3.
XX OS Homo sapiens.
XX PN WO200183555-A2.
XX PD 08-NOV-2001.
XX PF 04-MAY-2001; 2001WO-US014519.
XX PR 04-MAY-2000; 2000US-0202027P.
XX PR 01-AUG-2000; 2000US-0222344P.
XX PR 03-NOV-2000; 2000US-00704707.
XX PR 19-APR-2001; 2001US-0285493P.
XX PA (CALY ) CALIFORNIA INST OF TECHNOLOGY.
XX PI Anderson DJ, Dong X, Zylka M, Han S, Simon M;
XX WPI; 2002-171346/22.
XX N-PSDB; AAD33751.
XX DR
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XX Isolated polypeptide, Mr_g, which is a G-protein coupled receptor and an
PT isolated polypeptide, drg-12, which is also a receptor, useful for
PT identifying agonists or antagonists for treating pain.
XX
XX
PS Claim 16; Page 130; 185pp; English.

CC The invention relates to Mr_g (mas-related gene) protein, which is a G-
CC protein coupled receptor and drg-12 protein, which is a receptor. The
CC invention is useful for identifying compounds that bind to it, especially
CC agonists or antagonists. Administration of an agent (e.g. the identified
CC agonist) that increases the expression of Mr_g in a mammal may be used for
CC treating impaired sensory perception in a mammal, especially pain. The
CC antagonist may also be useful for treating impaired sensory perception in
CC a mammal. The present sequence is human Mr_gX3 protein

XX SQ Sequence 322 AA;

Query Match 100.0%; Score 1688; DB 5; Length 322;
Best Local Similarity 100.0%; Pred. No. 2e-174;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSTIPVLGTELPINGREETPCYKQTLSTGLTCTIVSLVLTGNVAVLWLLGCRMRNA 60
DB 1 MDSTIPVLGTELPINGREETPCYKQTLSTGLTCTIVSLVLTGNVAVLWLLGCRMRNA 60

QY 61 VSIYILNLVAADFLSGHICSPRLNIRHPISKILSPVMTFFYFGLSMLSAISTER 120
DB 61 VSIYILNLVAADFLSGHICSPRLNIRHPISKILSPVMTFFYFGLSMLSAISTER 120

QY 121 CLSILWPIWYHCRPRYLSVVMCVLLWALSILRSILEWPCDFLFGADSVWCETSDFIT 180
DB 121 CLSILWPIWYHCRPRYLSVVMCVLLWALSILRSILEWPCDFLFGADSVWCETSDFIT 180

QY 181 IAWLVFLCVLGGSSLLVRLICGSRKMPLETLVYLLTVLVLGCPFGIOWALFS 240
DB 181 IAWLVFLCVLGGSSLLVRLICGSRKMPLETLVYLLTVLVLGCPFGIOWALFS 240

QY 241 RIHLDMKVLFCFHVHLSIFLSALNSSANPIYFFVGSFRQRONRQNLKVLQALQDTPE 300
DB 241 RIHLDMKVLFCFHVHLSIFLSALNSSANPIYFFVGSFRQRONRQNLKVLQALQDTPE 300

QY 301 VDEGGWLPQETLELSGRLEQ 322

DB 301 VDEGGWLPQETLELSGRLEQ 322

RESULT 4

ID ABP81750 standard; protein; 322 AA.

AC ABP81750;

DT 04-MAR-2003 (first entry)

DE Human G protein-coupled receptor Mr_gX3 protein SEQ ID NO:674.

XX G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW G protein-coupled receptor modulator; antibody; immune-related disease;
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW immunological-related cell proliferative disease; autoimmune disease;
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KW ulcer.

OS Homo sapiens.

FN WO200261087-A2.

XX

PD 08-AUG-2002.

XX 19-DEC-2001; 2001WO-US050107.

XX 19-DEC-2000; 2000US-0257144P.

XX (LIFE-) LIFESPAN BIOSCIENCES INC.

XX Burner GC, Roush CL, Brown JP;

XX WPI; 2003-046718/04.

XX N-PSDB; ABZ42595.

PT New isolated antigenic peptides e.g., for G protein-coupled receptors
PT (GPCR), useful for diagnosing and designing drugs for treating conditions
PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
PT autoimmune diseases.

XX Disclosure; Fig 1; 523pp; English.

CC The present invention describes antigenic peptides (I) comprising: (a)
CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC acids. Also described: (1) an assay for the detection of a particular G
CC protein-coupled receptor (GPCR) or a candidate polypeptide in sample, or
CC and (2) an isolated antibody having high specificity and high affinity or
CC avidity for a particular GPCR. (1) can be used as GPCR modulators and in
CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
CC antibody against a particular GPCR, and in the production of specific
CC antibodies. The peptides and antibodies are also useful for detecting the
CC presence or absence of corresponding GPCRs. The antigenic peptides for
CC GPCRs and antibodies are useful for diagnosing and designing drugs for
CC treating immune-related diseases, growth-related diseases, cell
CC regeneration-related diseases, immunological-related cell proliferative
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC inflammation, allergies, Crohn's disease, diabetes, psoriasis, Crohn's
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC any other disorder in which GPCRs are involved. The antibodies may be
CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC exemplification of the present invention

XX SQ Sequence 322 AA;

Query Match 100.0%; Score 1688; DB 6; Length 322;

Best Local Similarity 100.0%; Pred. No. 2e-174;

Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSTIPVLGTELPINGREETPCYKQTLSTGLTCTIVSLVLTGNVAVLWLLGCRMRNA 60

DB 1 MDSTIPVLGTELPINGREETPCYKQTLSTGLTCTIVSLVLTGNVAVLWLLGCRMRNA 60

QY 61 VSIYILNLVAADFLSGHICSPRLNIRHPISKILSPVMTFFYFGLSMLSAISTER 120

DB 61 VSIYILNLVAADFLSGHICSPRLNIRHPISKILSPVMTFFYFGLSMLSAISTER 120

QY 121 CLSILWPIWYHCRPRYLSVVMCVLLWALSILRSILEWPCDFLFGADSVWCETSDFIT 180

DB 121 CLSILWPIWYHCRPRYLSVVMCVLLWALSILRSILEWPCDFLFGADSVWCETSDFIT 180

QY 181 IAWLVFLCVLGGSSLLVRLICGSRKMPLETLVYLLTVLVLGCPFGIOWALFS 240

DB 181 IAWLVFLCVLGGSSLLVRLICGSRKMPLETLVYLLTVLVLGCPFGIOWALFS 240

QY 241 RIHLDMKVLFCFHVHLSIFLSALNSSANPIYFFVGSFRQRONRQNLKVLQALQDTPE 300

DB 241 RIHLDMKVLFCFHVHLSIFLSALNSSANPIYFFVGSFRQRONRQNLKVLQALQDTPE 300

QY 301 VDEGGWLPQETLELSGRLEQ 322

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Db      301 VDEGGGWLPGQETLELSGSRLAQ 322
|||||
RESULT 5
AAU97598
ID AAU97598 standard; protein; 337 AA.
XX AC AAU97598;
XX DT 12-AUG-2002 (first entry)
XX DE Human G-protein coupled receptor (GPCR).
XX KW Human G-protein coupled receptor; GPCR; human protease;
XX KW human therapeutic protein; query sequence; search; chromosome 3;
XX KW sequence database; non-human transgenic animal; gene therapy.
XX OS Homo sapiens.
XX FH Key
XX FT Domain 41..61 Location/Qualifiers
XX FT Domain /label= Helix_1
XX FT Domain 75..95
XX FT Domain /label= Helix_2
XX FT Domain 112..132
XX FT Domain /label= Helix_3
XX FT Modified-site 133..135 /note=Protein kinase C (PKC) phosphorylation site"
XX FT Domain 151..171
XX FT Modified-site 169..172 /label= Helix_4
XX FT Modified-site 181..184 /note="Casein kinase II (CK2) phosphorylation site"
XX FT Domain 193..213 /note="Casein kinase II (CK2) phosphorylation site"
XX FT Modified-site 221..223 /label= Helix_5
XX FT Domain 229..249 /note="Protein kinase C (PKC) phosphorylation site"
XX FT Modified-site 244..249 /label= Helix_6
XX FT Modified-site 248..253 /note="Myristoylation site"
XX FT Modified-site 261..281 /note="Myristoylation site"
XX FT Modified-site 279..282 /label= Helix_7
XX FT Modified-site 292..294 /note="Asn glycosylation site"
XX FT Modified-site 333..336 /note="Protein kinase C (PKC) phosphorylation site"
XX FT Modified-site 333..336 /note="Casein kinase II (CK2) phosphorylation site"
XX FN WO200234914-A1.
XX XX
XX PD 02-MAY-2002.
XX PF 10-OCT-2001; 2001WO-US031592.
XX PR 25-OCT-2000; 2000US-00695045.
XX PR 31-MAY-2001; 2001US-00867570.
XX XX
XX PA (PEKE ) PE CORP NY.
XX XX
XX PI Wei M, Zhao Q, Woodage T, Di Francesco V, Beasley EM;
XX PI WPI; 2002-463360/49.
XX DR N-PSDB; ABK52822, ABK52823.
XX DR
XX XX
XX PT Novel isolated G-protein coupled receptor peptide useful for treating
XX PT disorder characterized by absence of, in appropriate or unwanted
XX PT expression of the receptor protein, and as immunogens to raise

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PT antibodies.
XX Claim 1; Fig 2; 75pp; English.
XX
CC The present invention relates to a new G-protein coupled receptor (GPCR)
CC peptide. The invention is useful for identifying a modulator of GPCR and
CC for treating a disease or condition mediated by a human protease. The
CC invention is also useful as models for the development of human
CC therapeutics, for identifying therapeutic proteins, as targets for
CC development of human therapeutic agents, and as query sequences to perform
CC a search against sequence databases to, for e.g., identify other family
CC members of related sequences. The vector of the invention is useful for
CC producing a GPCR protein or peptide, for conducting cell-based assays
CC involving a GPCR protein or its fragment, for identifying GPCR protein
CC mutants whose functions are affected, and to produce non-human transgenic
CC animals. The present amino acid sequence represents the human G-protein
CC coupled receptor (GPCR) protein of the invention. This sequence is
CC encoded by the human G-protein coupled receptor (GPCR) gene located on
CC chromosome 3
XX
XX SQ Sequence 337 AA;
Query Match 100.0%; Score 1688; DB 5; Length 337;
Best Local Similarity 100.0%; Pred. No. 2.1e-174;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDSTIPVLGTELTINGREETPCYKQTLSTGLTCTIVSLVALTGNVAVLLGCRMRNA 60
DB 16 MDSTIPVLGTELTINGREETPCYKQTLSTGLTCTIVSLVALTGNVAVLLGCRMRNA 75
QY 61 VSIYILNVAADFLFLSGHIICSPRLINIRHPISKILSPVMTFPYFGLSMLSAISTER 120
DB 76 VSIYILNVAADFLFLSGHIICSPRLINIRHPISKILSPVMTFPYFGLSMLSAISTER 135
QY 121 CLSTILWPIWYHCRPRYLSSVMCVLLWALSLLRSILEWMECDFLFGADSVWCETSDFIT 180
DB 136 CLSTILWPIWYHCRPRYLSSVMCVLLWALSLLRSILEWMECDFLFGADSVWCETSDFIT 195
QY 181 IAWLVFLCVLGCSSLLVLRILCGSRKNPLTRLYVTILTVLVLVLCGLPFGIOWALFS 240
DB 196 IAWLVFLCVLGCSSLLVLRILCGSRKNPLTRLYVTILTVLVLVLCGLPFGIOWALFS 255
QY 241 RIHLDWKVLFCHVHVSIFLSALNSSANPIIYFVGSFRORONRQNLKVLQALQDTPE 300
DB 256 RIHLDWKVLFCHVHVSIFLSALNSSANPIIYFVGSFRORONRQNLKVLQALQDTPE 315
QY 301 VDEGGGWLPGQETLELSGSRLAQ 322
DB 316 VDEGGGWLPGQETLELSGSRLAQ 337
RESULT 6
AAU90762
ID AAU90762 standard; protein; 322 AA.
XX AC AAU90762;
XX DT 18-AUG-2000 (first entry)
XX DE Human G protein-coupled receptor hHI7T213V SEQ ID NO.2.
XX KW Human; G protein-coupled receptor; hippocampus; diagnosis; screening;
XX KW genetic disease; cellular function regulation.
XX OS Homo sapiens.
XX XX
XX PN WO200020455-A1.
XX PD 13-APR-2000.
XX PF 30-SEP-1999; 99WO-JP005366.
XX PR 01-OCT-1998; 98JP-00279535.

```


XX (TAKE) TAKEDA CHEM IND LTD.
 XX PA Watanabe T, Terao Y, Matsui H;
 XX PI
 XX PF
 XX DR WPI; 2000-303747/26.
 XX DR N-PSDB; AAA29812.
 XX
 XX Human-derived G protein-coupled protein and encoding nucleic acid, useful
 XX PT e.g. in determining ligands and treatment of diseases associated with
 XX PT dysfunction of the protein.
 XX
 XX Claim 2; Page 92-93; 97pp; Japanese.
 XX
 XX The present sequence represents a human-derived G protein-coupled protein
 XX CC designated hH17T213V, which is isolated from the human hippocampus. The G
 XX CC protein-coupled receptor can be used for preventing, treating and
 XX CC diagnosing genetic diseases associated with G protein-coupled protein,
 XX CC and for regulating cellular functions. The protein can be used to prevent
 XX CC and treat disorders associated with G protein-coupled protein gene
 XX CC dysfunction. It can also be used to identify G protein-coupled protein
 XX CC ligands and generating antibodies and antisera against the protein. It is
 XX CC also useful in constructing recombinant receptor protein expression
 XX CC systems, developing receptor-binding assay systems and screening drug
 XX CC candidates, and can be used as a probe in the genetic diagnosis of G
 XX CC protein-coupled protein disorders
 XX
 XX Sequence 322 AA;
 SQ
 Query Match 99.7%; Score 1683; DB 3; Length 322;
 Best Local Similarity 99.7%; Pred. No. 6.8e-174;
 Matches 321; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDSTIPVLGTETLPINGREETPCYKQTLSTGLTCTIVSLVALTGNVAVLWLLGCRMRNA 60
 DB 1 MDSTIPVLGTETLPINGREETPCYKQTLSTGLTCTIVSLVALTGNVAVLWLLGCRMRNA 60
 QY 61 VSIYILNLVAADFLLSGHIIICSPRLINIRHPISKILSPVMTFFYFIGLSMLSAISTER 120
 DB 61 VSIYILNLVAADFLLSGHIIICSPRLINIRHPISKILSPVMTFFYFIGLSMLSAISTER 120
 QY 121 CLSILWPIWYHCRPRYLSSVMCVLLWALSLSRILEWFCDFLFGADSVWCETSDFIT 180
 DB 121 CLSILWPIWYHCRPRYLSSVMCVLLWALSLSRILEWFCDFLFGADSVWCETSDFIT 180
 QY 181 IAWLVFLCVVLCGSSLLVRLICGSRKMPLTRLYVTILLTVLVFLLCGLPFGIOWALFS 240
 DB 181 IAWLVFLCVVLCGSSLLVRLICGSRKMPLTRLYVTILLTVLVFLLCGLPFGIOWALFS 240
 QY 241 RIHLDWKVLFCHVHLVSIIFLSALNSSANPIIYFFVGSFRQRQRNQLKVLQALQDTPE 300
 DB 241 RIHLDWKVLFCHVHLVSIIFLSALNSSANPIIYFFVGSFRQRQRNQLKVLQALQDTPE 300
 QY 301 VDEGGGWLPQETLELSGRLEQ 322
 DB 301 VDEGGGWLPQETLELSGRLEQ 322
 RESULT 7
 ADC86821
 ID ADC86821 standard; protein; 322 AA.
 XX
 XX AC ADC86821;
 XX
 XX DT 01-JAN-2004 (first entry)
 XX
 XX DE Human GPCR protein SEQ ID NO:1274.
 XX
 XX KW human; GPCR; guanosine triphosphate-binding protein coupled receptor;
 XX gene therapy.
 XX
 XX OS Homo sapiens.

FN EF1270724-A2.
 XX
 XX PD 02-JAN-2003.
 XX
 XX PF 18-JUN-2002; 2002EP-00013517.
 XX
 XX PR 18-JUN-2001; 2001JP-00246789.
 XX
 XX PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
 XX PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
 XX
 XX PI Suwa M, Asai K, Akiyama Y, Aburatani H;
 XX
 XX WPI; 2003-315783/31.
 XX DR N-PSDB; ADC86820.
 XX
 XX New polynucleotide, useful for preparing a composition for treating a
 XX PT patient in need of increased or suppressed activity or expression of the
 XX PT guanosine triphosphate-binding protein coupled receptor.
 XX
 XX Claim 2; SEQ ID NO 1274; 28pp; English.
 XX
 XX The invention relates to a novel polynucleotide encoding a guanosine
 XX CC triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of
 XX CC the invention may have a use in gene therapy. The polynucleotide and
 XX CC polypeptide are useful for preparing a composition for treating a patient
 XX CC in need of increased or suppressed activity or expression of the
 XX CC guanosine triphosphate-binding protein coupled receptor. The protein
 XX CC sequences shown in ADC85549-ADC87617 represent GPCR's of the invention.
 XX
 XX Sequence 322 AA;
 SQ
 Query Match 99.7%; Score 1683; DB 7; Length 322;
 Best Local Similarity 99.7%; Pred. No. 6.8e-174;
 Matches 321; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDSTIPVLGTETLPINGREETPCYKQTLSTGLTCTIVSLVALTGNVAVLWLLGCRMRNA 60
 DB 1 MDSTIPVLGTETLPINGREETPCYKQTLSTGLTCTIVSLVALTGNVAVLWLLGCRMRNA 60
 QY 61 VSIYILNLVAADFLLSGHIIICSPRLINIRHPISKILSPVMTFFYFIGLSMLSAISTER 120
 DB 61 VSIYILNLVAADFLLSGHIIICSPRLINIRHPISKILSPVMTFFYFIGLSMLSAISTER 120
 QY 121 CLSILWPIWYHCRPRYLSSVMCVLLWALSLSRILEWFCDFLFGADSVWCETSDFIT 180
 DB 121 CLSILWPIWYHCRPRYLSSVMCVLLWALSLSRILEWFCDFLFGADSVWCETSDFIT 180
 QY 181 IAWLVFLCVVLCGSSLLVRLICGSRKMPLTRLYVTILLTVLVFLLCGLPFGIOWALFS 240
 DB 181 IAWLVFLCVVLCGSSLLVRLICGSRKMPLTRLYVTILLTVLVFLLCGLPFGIOWALFS 240
 QY 241 RIHLDWKVLFCHVHLVSIIFLSALNSSANPIIYFFVGSFRQRQRNQLKVLQALQDTPE 300
 DB 241 RIHLDWKVLFCHVHLVSIIFLSALNSSANPIIYFFVGSFRQRQRNQLKVLQALQDTPE 300
 QY 301 VDEGGGWLPQETLELSGRLEQ 322
 DB 301 VDEGGGWLPQETLELSGRLEQ 322
 RESULT 8
 AAB14846
 ID AAB14846 standard; protein; 322 AA.
 XX
 XX AC AAB14846;
 XX
 XX DT 19-DEC-2000 (first entry)
 XX
 XX DE Human novel G-protein coupled receptor #1.
 XX
 XX KW Human; novel G-protein coupled receptor; signal transduction;
 XX disease diagnosis; drug screening; disease therapy.

XX OS Homo sapiens.
 XX PN W0200040724-A1.
 XX PD 13-JUL-2000.
 XX PF 04-JAN-2000; 2000WO-US0000052.
 XX PR 04-JAN-1999; 99US-0114566P.
 XX PR 14-JAN-1999; 99US-0115828P.
 XX PA (LEXI-) LEXICON GENETICS INC.
 XX PI Nehls M, Wattler F;
 XX DR WPI; 2000-465986/40.
 XX DR N-PSDB; AAA70342.
 XX FT New polynucleotides encoding novel G-protein coupled receptors useful for
 PT diagnosis, drug screening, clinical trial monitoring and for the
 PT treatment of physiological or behavioral disorders.
 XX PS Claim 1; Page 53-54; 61pp; English.
 XX CC The present sequence is the protein sequence for a novel human G-protein
 CC coupled receptor (NGPCR). These proteins are involved in signal
 CC transduction pathways in many cases. The protein contains seven
 CC transmembrane domains, and is expressed in human testis, mammary gland
 CC and salivary gland tissue. The protein, its gene, agonists, antagonists
 CC and antibodies can be used to diagnose and treat diseases associated with
 CC the inappropriate expression or expression of mutant versions of the
 CC protein, for screening for drugs which can be used in the same manner,
 CC and for elucidating the function of the protein.
 XX SQ Sequence 322 AA;
 Query Match 98.5%; Score 1663; DB 3; Length 322;
 Best Local Similarity 99.4%; Pred. No. 1e-171;
 Matches 320; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MDSTIPVLGTELTIPINGREETPCYKQTLSTGLTCTIVSLVALTGNVAVLLGCMRRA 60
 DB 1 MDSTIPVLGTELTIPINGREETPCYKQTLSTGLTCTIVSLVALTGNVAVLLGCMRRA 60
 QY 61 VSIYILNLVAADFLSGHIICSPRLINIRHPISKILSPVMTFPFYFGLSMLSAISTER 120
 DB 61 VSIYILNLVAADFLSGHIIRSPRLINIRHPISKILSPVMTFPFYFGLSMLSAISTER 120
 QY 121 CLSILWPIWYHCRPRYLSSVMCVLLWALSILRSILEWMCDFLFGADSVWCETSDFIT 180
 DB 121 CLSILWPIWYHCRPRYLSSVMCVLLWALSILRSILEWMCDFLFGADSVWCETSDFIT 180
 QY 181 IAWLVFLCVLGGSSVLVRLICGSRKMPLTRIVVTLTLLTVLFLCGLPFGIQWALFS 240
 DB 181 IAWLVFLCVLGGSSVLVRLICGSRKMPLTRIVVTLTLLTVLFLCGLPFGIQWALFS 240
 QY 241 RIHLWKVLFCHVHLVSIPLSALNSSANPIIYFFVGSFRQNRQNLKVLQALQDTP 300
 DB 241 RIHLWKVLFCHVHLVSIPLSALNSSANPIIYFFVGSFRQNRQNLKVLQALQDTP 300
 QY 301 VDEGGWLPQETLELSGSRLEQ 322
 DB 301 VDEGGWLPQETLELSGSRLEQ 322
 RESULT 9
 ID AAY30159 standard; protein; 322 AA.
 XX AC AAY30159;
 XX DT 20-MAR-2003 (revised)

DT 26-NOV-1999 (first entry)
 XX Human dorsal root receptor 1 hDRR1.
 XX KW Dorsal root receptor; dorsal root ganglia; G-protein coupled receptor;
 XX KW hDRR1; central nervous system; CNS; anaesthesia; analgesia; neuron; pain.
 XX OS Homo sapiens.
 XX PN W09932519-A1.
 XX PD 01-JUL-1999.
 XX PF 16-DEC-1998; 98WO-SE002348.
 XX PR 22-DEC-1997; 97SE-00004836.
 XX PA (ASTR) ASTRA PHARMA INC.
 XX PA (ASTR) ASTRA AB.
 XX PI Ahmad S, Banville D, Fortin Y, Lembo P, O'donnell D, Shen S;
 XX DR WPI; 1999-405162/34.
 XX DR N-PSDB; AAZ10067.
 XX FT Rat and human dorsal root receptors and related polynucleotides, useful
 PT for identifying agents for anesthesia and analgesia.
 XX PS Claim 6; Page 39-41; 72pp; English.
 XX CC This is the human dorsal root receptor 1 (hDRR1) protein sequence. This
 CC is a G protein coupled receptor that is expressed preferentially in
 CC dorsal root ganglia. hDRR1 can be used to create antibodies against
 CC hDRR1. The dorsal root ganglia area of the central nervous system (CNS)
 CC is densely innervated with primary or afferent neurons involved in
 CC transmission, modulation and sensation of pain. The DR's which are
 CC expressed in this region of the CNS may be used for assays for the
 CC identification of new agents for anaesthesia and analgesia. (Updated on
 CC 20-MAR-2003 to correct PA field.)
 XX SQ Sequence 322 AA;
 Query Match 97.3%; Score 1642; DB 2; Length 322;
 Best Local Similarity 97.2%; Pred. No. 1.9e-169;
 Matches 313; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
 QY 1 MDSTIPVLGTELTIPINGREETPCYKQTLSTGLTCTIVSLVALTGNVAVLLGCMRRA 60
 DB 1 MDSTIPVLGTELTIPINGREETPCYKQTLSTGLTCTIVSLVALTGNVAVLLGCMRRA 60
 QY 61 VSIYILNLVAADFLSGHIICSPRLINIRHPISKILSPVMTFPFYFGLSMLSAISTER 120
 DB 61 VSIYILNLVAADFLSGHIIFSPRLINIRHPISKILSPVMTFPFYFGLSMLSAISTER 120
 QY 121 CLSILWPIWYHCRPRYLSSVMCVLLWALSILRSILEWMCDFLFGADSVWCETSDFIT 180
 DB 121 CLSILWPIWYHCRPRYLSSVMCVLLWALSILRSILEWMCDFLFGADSVWCETSDFIT 180
 QY 181 IAWLVFLCVLGGSSVLVRLICGSRKMPLTRIVVTLTLLTVLFLCGLPFGIQWALFS 240
 DB 181 IAWLVFLCVLGGSSVLVRLICGSRKMPLTRIVVTLTLLTVLFLCGLPFGIQWALFS 240
 QY 241 RIHLWKVLFCHVHLVSIPLSALNSSANPIIYFFVGSFRQNRQNLKVLQALQDTP 300
 DB 241 RIHLWKVLFCHVHLVSIPLSALNSSANPIIYFFVGSFRQNRQNLKVLQALQDTP 300
 QY 301 VDEGGWLPQETLELSGSRLEQ 322
 DB 301 VDEGGWLPQETLELSGSRLEQ 322
 RESULT 10
 AAY30160

AA30160 standard; protein; 322 AA.
AA30160;
20-MAR-2003 (revised)
26-NOV-1999 (first entry)
Human dorsal root receptor 2 hRR2.
Dorsal root receptor; dorsal root ganglia; G-protein coupled receptor;
hRR2; central nervous system; CNS; anaesthesia; analgesia; neuron; pain.
Homo sapiens.
WO9932519-A1.
01-JUL-1999.
16-DEC-1998; 98WO-SE002348.
22-DEC-1997; 97SE-00004836.
(ASTR) ASTRA PHARMA INC.
(ASTR) ASTRA AB.
Ahmad S, Barville D, Fortin Y, Lembo P, O'donnell D, Shen S;
WPI; 1999-405162/34.
DR N-PSDB; AA210068.
Rat and human dorsal root receptors and related polynucleotides, useful
for identifying agents for anaesthesia and analgesia.
Claim 11; Page 43-45; 72pp; English.
This is the human dorsal root receptor 2 (hRR2) protein sequence. This
is a G protein coupled receptor that is expressed preferentially in
dorsal root ganglia. hRR2 can be used to create antibodies against
hRR2. The dorsal root ganglia area of the central nervous system (CNS)
is densely innervated with primary or afferent neurons involved in
transmission, modulation and sensation of pain. The DR's which are
expressed in this region of the CNS may be used for assays for the
identification of new agents for anaesthesia and analgesia. (Updated on
20-MAR-2003 to correct PA field.)
Sequence 322 AA;
Query Match 94.7%; Score 1598; DB 2; Length 322;
Best Local Similarity 95.6%; Pred. No. 1.2e-164; Mismatches 9; Indels 0; Gaps 0;
Matches 307; Conservative 5;
QY 1 MDSTIPVLGTLPINGREETPCYKQTLSTGLTCTIVSLVALTGNNAVVLWLLGCRMRNA 60
DB 1 MDPTVPVLGTLPINGREETPCYKQTLSTGLTCTIVSLVALTGNNAVVLWLLGCRMRNA 60
QY 61 VSIYILNLVAADFLFSGHIIICSPRLINIRHPISKILSPWMTFFYFGLSMLSAISTER 120
DB 61 VSIYILNLVAADFLFSGHIIICSPRLINIRHPISKILSPWMTFFYFGLSMLSAISTER 120
QY 121 CLSILWPIWYHCRPRYLSVMCVLLWALSILRSILEWFCDFLFGADSVWCETSDFIT 180
DB 121 CLSILWPIWYHCRPRYLSVMCVLLWALSILRSILEWFCDFLFGADSVWCETSDFIT 180
QY 181 IAWLVLCVVLGSSILVLRILCGSRKMPRLRYVITLLTVLVFLLCGLPFGIOWALFS 240
DB 181 IAWLVLRVLCGSSILVLRILCGSRKMPRLRYVITLLTVLVFLLCGLPFGIOWALFS 240
QY 241 RIHLWKVLFCHVHLVSIIFLSALNSSANPIIYFFVGSFRQNRQNLKVLQRLQDTPE 300
DB 241 RIHLWKVLFCHVHLVSIIFLSALNSSANPIIYFFVGSFRQNLKVLQRLQDTPE 300
QY 301 VDEGGWLPQETLELSGSKLE 321
|||||

DB 301 VDEGGWLPQETLELSGSKLE 321
RESULT 11
ABP96695
ID ABP96695 standard; protein; 302 AA.
XX AC ABP96695;
XX DT 03-JUN-2003 (first entry)
XX DE Human G protein-coupled receptor DRG7 protein SEQ ID NO:10.
XX KW Human; G protein-coupled receptor; GPCR; DRG; pain; sensory transduction.
XX OS Homo sapiens.
XX PN WO2003023010-A2.
XX PD 20-MAR-2003.
XX PF 06-SEP-2002; 2002WO-US028619.
XX PR 07-SEP-2001; 2001US-0317879P.
XX PA (IRMI-) IRM LLC.
XX PI Liao J, Gray NS, Caldwell JC, Schultz PG;
XX DR N-PSDB; ACC44771.
XX PT Novel G-protein coupled receptor polypeptide expressed in mammalian
sensory neurons of dorsal root ganglia, useful as target for screening
for agents that regulate pain.
XX PS Claim 10; Page 50; 51pp; English.
XX CC The present invention describes human G protein-coupled receptor (GPCR)
proteins (I) designated DRG1, DRG2, DRG4, DRG6, DRG7, and DRG8 (see
ASP96691 to ABP96696) encoded by ACC44767 to ACC44772. (I) can be used
for identifying a compound that modulates pain, by contacting a compound
with (I), and selecting a compound that binds to the extracellular domain
of that modulates GPCR activity of the polypeptide. Such compounds that
modulate the activity of (I) can be used to investigate the role of (I)
in sensory (e.g. pain) transduction. Biologically active (I) can be used
for testing inhibitors and activators of (I) as pain transducers or pain
inhibitors using in vivo and in vitro expression that measure e.g.
transcriptional activation of (I), ligand binding, phosphorylation and
dephosphorylation, binding to G-proteins, G-protein activation,
regulatory molecule binding, voltage, membrane potential and conductance
changes, ion flux, intracellular second messengers such as cAMP and
inositol triphosphate, intracellular calcium levels and neurotransmitter
release. Such activators and inhibitors identified using (I) can be used
to further study sensory transduction and to identify specific pain
agonists and antagonists. The modulators can be administered directly to
the mammalian subject for modulation of pain in vivo
Sequence 302 AA;
Query Match 92.2%; Score 1557; DB 6; Length 302;
Best Local Similarity 93.5%; Pred. No. 3e-160;
Matches 301; Conservative 1; Mismatches 0; Indels 20; Gaps 1;
QY 1 MDSTIPVLGTLPINGREETPCYKQTLSTGLTCTIVSLVALTGNNAVVLWLLGCRMRNA 60
DB 1 MDSTIPVLGTLPINGREETPCYKQTLSTGLTCTIVSLVALTGNNAVVLWLLGCRMRNA 40
QY 61 VSIYILNLVAADFLFSGHIIICSPRLINIRHPISKILSPWMTFFYFGLSMLSAISTER 120
DB 41 VSIYILNLVAADFLFSGHIIICSPRLINIRHPISKILSPWMTFFYFGLSMLSAISTER 100
QY 121 CLSILWPIWYHCRPRYLSVMCVLLWALSILRSILEWFCDFLFGADSVWCETSDFIT 180
|||||

Db 101 CUSILPWIYHCRPRYLSSVMCVLLWALSLSRSLRWFCDFLFGANSVWCETSDFIT 160
QY 181 IAWLVFLCVVLCGSSLVLLVRLILCGSRKMPRLTYVITLLTVLVFLCGLPFGIQWALFS 240
Db 161 IAWLVFLCVVLCGSSLVLLVRLILCGSRKMPRLTYVITLLTVLVFLCGLPFGIQWALFS 220
QY 241 RIHLDMKVLFCVHLVSIIFLSALNSSANPIIYFFVGSFRQRNRLKLVLRALQDTPE 300
Db 221 RIHLDMKVLFCVHLVSIIFLSALNSSANPIIYFFVGSFRQRNRLKLVLRALQDTPE 280
QY 301 VDEGGWLPQETLELSGSRLQ 322
Db 281 VDEGGWLPQETLELSGSRLQ 302

RESULT 12
AA30161
ID RAY30161 standard; protein; 322 AA.

AC AA30161;
XX
XX
DT 20-MAR-2003 (revised)
DT 26-NOV-1999 (first entry)
XX
XX
DE Human dorsal root receptor 3 hDRR3.
XX
XX Dorsal root receptor; dorsal root ganglia; G-protein coupled receptor;
KW hDRR3; central nervous system; CNS; anaesthesia; analgesia; neuron; pain.
XX
CS Homo sapiens.
XX
XX WO9932519-A1.
XX
XX 01-JUL-1999.
XX
XX 16-DEC-1998; 98WO-SE002348.
XX
XX 22-DEC-1997; 97SE-00004836.
XX
XX (ASTR) ASTRA PHARMA INC.
XX (ASTR) ASTRA AB.
XX
XX Ahmad S, Banville D, Fortin Y, Lembo P, O'donnell D, Shen S;
XX
XX WPI; 1999-405162/34.
XX N-PSDB; AAZ10069.
XX
XX Rat and human dorsal root receptors and related polynucleotides, useful
XX for identifying agents for anesthesia and analgesia.
XX
XX Claim 16; Page 48-50; 72pp; English.

XX This is the human dorsal root receptor 3 (hDRR3) protein sequence. This
XX is a G protein coupled receptor that is expressed preferentially in
XX dorsal root ganglia. hDRR3 can be used to create antibodies against
XX hDRR3. The dorsal root ganglia area of the central nervous system (CNS)
XX is densely innervated with primary or afferent neurons involved in
XX transmission, modulation and sensation of pain. The DRR's which are
XX expressed in this region of the CNS may be used for assays for the
XX identification of new agents for anaesthesia and analgesia. (Updated on
XX 20-MAR-2003 to correct PA field.)
XX

SQ Sequence 322 AA;
Query Match 83.2%; Score 1405; DB 2; Length 322;
Best Local Similarity 83.9%; Pred. No. 1e-143;
Matches 270; Conservative 18; Mismatches 34; Indels 0; Gaps 0;

QY 1 MDSTIPVLGTLPINGRETFPCYKQLSFTGLCTIVSLVALTGNAVVLMLGCRMRNA 60
Db 1 MDPTVSTLDTLTPINGTEETLCYKQLSFTGLCTIVSLVALTGNAVVLMLGCRMRNA 60

QY 61 VSIYILNVAADFLSLGHIICSPRLINIRHFIKILSPVMTFPYFIFGLSMLSAISTER 120
Db 61 FSIYILNVAADFLSLGRIIYLLSIFISPHITISKILYPMVFSYFAGLNFLSAVSTDR 120
QY 121 CLSILPWIYHCRPRYLSSVMCVLLWALSLSRSLRWFCDFLFGANSVWCETSDFIT 180
Db 121 CLSILPWIYHCRPRYLSSVMCVLLWALSLSRSLRWFCDFLFGANSVWCETSDFIT 160
QY 181 IAWLVFLCVVLCGSSLVLLVRLILCGSRKMPRLTYVITLLTVLVFLCGLPFGIQWALFS 240
Db 181 VAWIFLCVVCSSLVLLVRLILCGSRKIPRLTYVITLLTVLVFLCGLPFGIQWALFS 240
QY 241 RIHLDMKVLFCVHLVSIIFLSALNSSANPIIYFFVGSFRQRNRLKLVLRALQDTPE 300
Db 241 WIHVDREVLFCVHLVSIIFLSALNSSANPIIYFFVGSFRQRNRLKLVLRALQDTPE 300
QY 301 VDEGGWLPQETLELSGSRLQ 322
Db 301 VDEGGWLPQETLELSGSRLQ 322

RESULT 13
ADC12766
ID ADC12766 standard; protein; 304 AA.

XX ADC12766;
XX
XX 18-DEC-2003 (first entry)
XX
XX Human GPCR protein, SEQ ID NO 98.
XX
XX G protein-coupled receptor; GPCR; antibacterial; fungicide; protozoacide;
KW virucide; antirheumatic; antiarthritic; tranquiliser; antidiabetic;
KW osteopathic; nootropic; neuroprotective; anorectic; cardiant;
KW neuroleptic; cyostatic; antiparkinsonian; hypotensive; hypertensive;
KW antiulcer; antiallergic; anticonvulsant; analgesic; infection;
KW rheumatoid arthritis; chronic obstructive pulmonary diseases; COPD;
KW asthma; non-insulin dependent diabetes; obesity; osteoporosis;
KW Alzheimer's disease; age-related macular degeneration;
KW myocardial infarction; schizophrenia; osteoarthritis; cancer;
KW Parkinson's disease; congestive heart failure; hypotension; hypertension;
KW ulcer; allergy; benign prostatic hyperplasia; seizure disorder; anxiety;
KW obsessive compulsive disorder; Cushing's syndrome; hypopituitarism; pain;
XX human.
XX
XX Homo sapiens.
XX WO2003000893-A2.
XX
XX 03-JAN-2003.
XX
XX 24-JUN-2002; 2002WO-IB002357.
XX
XX 26-JUN-2001; 2001US-0301095P.
XX 06-NOV-2001; 2001US-0333185P.
XX
XX (DECO-) DECODE GENETICS EHF.
XX
XX Martinez RMA, Sigurdsson GT;
XX WPI; 2003-210155/20.
XX N-PSDB; ADC12765.
XX
XX New G protein-coupled receptor (GPCR) genes and polypeptides, useful for
XX diagnosing diseases associated with a GPCR, or in gene therapy for
XX treating e.g. obesity, osteoporosis, Alzheimer's, cancers or congestive
XX heart failure.
XX
XX Claim 10; SEQ ID NO 98; 253pp; English.
XX
XX The invention relates to a novel isolated nucleic acid of a G protein-
XX coupled receptor (GPCR) gene comprising any of 62 sequences of 312-2454
XX bp, or its complements; a GPCR polypeptide comprising any of 62 sequences

CC of 291-818 amino acids; or a nucleic acid that hybridises, under high
 CC stringency conditions, with any of the 62 GPCR sequences or any of their
 CC complements. The GPCR agents of the invention have the following
 CC activities: antibacterial, fungicide, protozoacide, virucide,
 CC antirheumatic, tranquiliser, antiarthritic, antidiabetic, osteopathic,
 CC neurotropic, neuroprotective, anorectic, cardiant, neuroleptic, cytostatic,
 CC antiparkinsonian, hypotensive, hypertensive, antiulcer, antiallergic,
 CC anticonvulsant, and analgesic. The GPCR therapeutic agent, particularly a
 CC GPCR gene agonist or antagonist, is useful for treating a disease or
 CC condition associated with a GPCR in an individual. The nucleic acid cited
 CC above, which is 100 or fewer nucleotides in length, is useful for
 CC assaying a sample for the presence of the GPCR gene nucleic acid or a
 CC GPCR gene nucleic acid with at least one nucleotide difference from a
 CC first nucleic acid, or for diagnosing a susceptibility to a disease or
 CC conditions associated with a GPCR. These diseases include infections
 CC (e.g. bacterial, fungal, protozoan or viral), rheumatoid arthritis,
 CC chronic obstructive pulmonary diseases (COPD), asthma, non-insulin
 CC dependent diabetes, obesity, osteoporosis, Alzheimer's disease, age-
 CC related macular degeneration, myocardial infarction, schizophrenia,
 CC osteoarthritis, cancers, Parkinson's diseases, congestive heart failure,
 CC hypertension, hypertension, ulcers, allergies, benign prostatic
 CC hyperplasia, seizure disorder, anxiety, obsessive compulsive disorder,
 CC Cushing's syndrome, hypopituitarism, or pain. This sequence represents
 CC one of the 62 GPCR proteins of the invention.
 XX
 SQ Sequence 304 AA;

Query Match 82.9%; Score 1399; DB 7; Length 304;

Best Local Similarity 99.6%; Pred. No. 4.3e-143;

Matches 266; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 23 CYKQLSFTGLTCIVSLVALTGNVAVLWLLGCMRRNAVSIYILNLVAADFLLSGHTIC 82
 DB 1 CYKQLSFTGLTCIVSLVALTGNVAVLWLLGCMRRNAVSIYILNLVAADFLLSGHTIC 60
 QY 83 SPLRLINRHPIKSLSPVMTFPYFGLSMLSAISTERCLSIPLWYCHRRPRLSSVM 142
 DB 61 SPLRLINRHPIKSLSPVMTFPYFGLSMLSAISTERCLSIPLWYCHRRPRLSSVM 120
 QY 143 CVELLWALSRLSILEWMECDFLFGSADSVWCETSDFTIAMLVLCVVLGSSLLVLR 202
 DB 121 CVELLWALSRLSILEWMECDFLFGSADSVWCETSDFTIAMLVLCVVLGSSLLVLR 180
 QY 203 LCGSRKMPLTRLYVILLTVLVFLVLCGLPFGIQWALFRIHLDKWLKVLCHVLSIFLSA 262
 DB 181 LCGSRKMPLTRLYVILLTVLVFLVLCGLPFGIQWALFRIHLDKWLKVLCHVLSIFLSA 240
 QY 263 LNSSANPIIYFFVGSFRQRQNLKL 289
 DB 241 LNSSANPIIYFFVGSFRQRQNLKL 267

RESULT 14

AY30162
 ID AAY30162 standard; protein; 322 AA.

XX
 AC AAY30162;

XX 20-MAR-2003 (revised)

DT 26-NOV-1999 (first entry)

XX Human dorsal root receptor 4 hDRR4.

DE Dorsal root receptor; dorsal root ganglia; G-protein coupled receptor;

KW hDRR4; central nervous system; CNS; anaesthesia; analgesia; neuron; pain.

XX Homo sapiens.

OS Homo sapiens.

PH Key Location/Qualifiers

FT Misc-difference 310 /note= "Encoded by GAC"

FT Misc-difference 312 /note= "Encoded by ATC"

FT

XX WO9932519-A1.
 PN 01-JUL-1999.
 PD 16-DEC-1998; 98WO-SE002348.
 PF 22-DEC-1997; 97SE-00004836.
 PR (ASTR) ASTRA PHARMA INC.
 XX (ASTR) ASTRA AB.
 PA Ahmad S, Banville D, Fortin Y, Lembo P, O'donnell D, Shen S;
 PI WPI; 1999-405162/34.
 XX N-PSDB; AA210070.
 DR Rat and human dorsal root receptors and related polynucleotides, useful
 PT for identifying agents for anaesthesia and analgesia.
 PT Claim 21; Page 52-54; 72pp; English.
 PS This is the human dorsal root receptor 4 (hDRR4) protein sequence. This
 CC is a G protein coupled receptor that is expressed preferentially in
 CC dorsal root ganglia. hDRR4 can be used to create antibodies against
 CC hDRR4. The dorsal root ganglia area of the central nervous system (CNS)
 CC is densely innervated with primary or afferent neurons involved in
 CC transmission, modulation and sensation of pain. The DRG's which are
 CC expressed in this region of the CNS may be used for assays for the
 CC identification of new agents for anaesthesia and analgesia. (Updated on
 CC 20-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 322 AA;

Query Match 82.4%; Score 1391; DB 2; Length 322;

Best Local Similarity 83.9%; Pred. No. 3.4e-142;

Matches 270; Conservative 16; Mismatches 36; Indels 0; Gaps 0;

QY 1 MDFTVPVLGTELPINGRBTCPYKQTLSTGLTCTIVSLVALTGNVAVLWLLGCMRRNA 60
 DB 1 MDFTVSLDTELPINGTEETLCYKQTLSTGLTCTIVSLVALTGNVAVLWLLGCMRRNA 60
 QY 61 VSIYILNLVAADFLLSGHTICSPBLINRHPIKSLSPVMTFPYFGLSMLSAISTER 120
 DB 61 FSIYILNLVAADFLLSGHTIYSLLSFISPHITISKILYPMVMFYSFAGLSFSLVSTER 120
 QY 121 CLSLTLPWYCHRRPRLSSVMCVLLWALSRLSILEWMECDFLFGSADSVWCETSDFIT 180
 DB 121 CLSLTLPWYCHRRPRLSSVMCVLLWALSRLSILEWMECDFLFGSADSVWCETSDFIT 180
 QY 181 IAWLVLCVVLGSSLLVLRILCGSRKMPLTRLYVILLTVLVFLVLCGLPFGIQWALFS 240
 DB 181 VAWLVLCVVLGSSLLVLRILCGSRKMPLTRLYVILLTVLVFLVLCGLPFGIQWALFS 240
 QY 241 RIHLDKWLKVLCHVLSIFLSALNSSANPIIYFFVGSFRQRQNLKLVLQALQDTP 300
 DB 241 WIHVDREVLCHVLSIFLSALNSSANPIIYFFVGSFRQRQNLKLVLQALQDASE 300
 QY 301 VDEGGWLPQETLELSGRLEQ 322
 DB 301 VDEGGWLPQETLELSGRLEQ 322

RESULT 15

AY87664

ID AAY87664 standard; protein; 322 AA.

XX AAY87664;

AC AAY87664;

XX 11-AUG-2000 (first entry)

DT Human G protein-coupled receptor protein #2.

XX

KW G protein-coupled receptor protein; human; treatment; diagnosis;
KW genetic disorder.

XX Homo sapiens.

XX WO200020456-A1.

XX PD 13-APR-2000.

XX PF 30-SEP-1999; 99WO-JP005365.

XX PR 01-OCT-1998; 98JP-00279512.

XX PR 20-OCT-1998; 98JP-00298667.

XX PA (TAKE) TAKEDA CHEM IND LTD.

XX PI Watanabe T, Terao Y, Fukusumi S;

XX WPI; 2000-303748/26.

XX N-PSDB; AAA12205.

XX Novel human-originated G protein-coupled protein and encoding nucleic
PT acid useful for e.g. identifying ligands and treating diseases
PT associated with dysfunction of the protein.

XX Claim 2; Page 97-98; 105pp; Japanese.

XX This invention describes a novel human G protein-coupled receptor protein
CC (1). The products of the invention can be used for preventing, treating
CC and diagnosing gene diseases and for regulating cellular functions. The
CC protein can be used to identify ligands and generate antibodies and
CC antisera. It is also useful in the construction of a recombinant receptor
CC protein expression system, developing a receptor-binding assay system and
CC screening drug candidates and as a probe in diagnosing genetic disorders
CC involving G protein-coupled protein. This sequence represents a human G-
CC protein coupled receptor protein described in the method of the invention
XX

SQ Sequence 322 AA;

Query Match 82.2%; Score 1387; DB 3; Length 322;
Best Local Similarity 84.1%; Pred. No. 9.4e-142;
Matches 269; Conservative 20; Mismatches 31; Indels 0; Gaps 0;
QY 1 MDSIPVLGTELTPINGREETPCYKQTLSTFTGLTCIVSLVALTGNAVLWLLGCRM RNA 60
DB 1 MDPTVPVLGKLTPIINGREETPCYKQTLSTFTGLTCIVSLVALTGNAVLWLLGCRM RNA 60
QY 61 VSIYILNLVAADFLFLSGHIICSPRLINIRHPISKILSPVMTFPYPFIGLSMLSAISTER 120
DB 61 VSIYILNLAAADFLFLSQIIRSPRLINIRHPISKILSPVMTFPYPFIGLSMLSAISTER 120
QY 121 CLSILMPWYHCRPRVYLSVWCVLLNALSLRSLRSLRSLRSLRSLRSLRSLRSLRSLRSLR 180
DB 121 CLSVLWPIWYRCRPTHTLSAVCVLLWGLSLFLSNLEWRFCDFLFGADSSWCETSDFI 180
QY 181 IAWLFLCVLSCGSSVLLVRLICGSRMPRLRYVLTLLTVLVLFCGLPFGIOWALFS 240
DB 181 VAWLFLCVLSCVSSVLLVRLICGSRMPRLRYVLTLLTVLVLFCGLPFGIOWALFS 240
QY 241 RIHLDKVLFCHVHLVSLFSLANSSANPIYFVGSFRQFQFQFQFQFQFQFQFQFQFQF 300
DB 241 RMHLNLEVLVCHVLCVMSLSLSSANPIYFVGSFRQFQFQFQFQFQFQFQFQFQFQF 300
QY 301 VDEGGWLPQETLELSGRL 320
DB 301 VDXGEGQLPEESLELSGRL 320

Search completed: July 4, 2004, 08:43:45
Job time : 78 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 4, 2004, 08:42:29 ; Search time 23 Seconds
(without alignments)
722.764 Million cell updates/sec

Title: US-09-787-879C-1
Perfect score: 1688
Sequence: 1 MDSIPVLGELTPINGREE.....EGGWLPEQTELSGSRLEQ 322

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	423.5	25.1	325	6	Patent No. 5320941-2
2	388.5	23.0	282	1	Sequence 52, Appl
3	388.5	23.0	282	5	PCT-US93-08528-52
4	344	20.4	298	1	Sequence 76, Appl
5	344	20.4	298	5	PCT-US93-08528-76
6	255.5	15.1	395	3	Sequence 6, Appl
7	255.5	15.1	395	3	US-08-981-825-6
8	235.5	14.0	354	1	US-07-759-568-2
9	226.5	13.4	355	1	US-07-759-568-1
10	226.5	13.4	355	2	US-08-450-393A-8
11	226.5	13.4	355	2	US-08-390-000A-5
12	226.5	13.4	355	3	US-08-448-669-8
13	226.5	13.4	355	5	PCT-US95-00476-8
14	226.5	13.4	360	1	US-08-202-056-7
15	226.5	13.4	360	4	US-09-409-778-4
16	219.5	13.0	369	1	US-07-816-283-8
17	219.5	13.0	369	1	US-08-417-103-8
18	219.5	13.0	369	2	US-08-411-859-3
19	219.5	13.0	369	3	US-08-120-601B-9
20	219.5	13.0	369	3	US-08-387-707-9
21	219.5	13.0	369	4	US-08-405-271A-9
22	211	12.5	353	4	US-09-576-160B-6
23	210	12.4	359	4	US-09-261-599B-3
24	210	12.4	359	4	US-09-456-455A-3
25	207.5	12.3	380	3	US-08-676-351-5
26	205.5	12.2	355	4	US-09-170-496D-2
27	205.5	12.2	384	3	US-09-071-434-3

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333 4 US-09-170-496D-8
333 4 US-09-170-496D-168
333 4 US-09-188-275A-5
380 4 US-09-351-198-5
380 4 US-09-113-426-5
381 1 US-08-467-125-2
381 2 US-08-911-320A-2
381 3 US-09-217-101-2
381 3 US-08-147-592A-2
380 4 US-08-292-694A-2
380 4 US-09-214-904-6
355 4 US-09-170-496D-164
380 1 US-08-149-093A-7
380 2 US-08-911-245-7
380 3 US-09-510-473-7
342 3 US-08-852-824-2
369 1 US-07-816-283-6
369 1 US-08-417-103-6

```

ALIGNMENTS

```

RESULT 1
5320941-2
; Patent No. 5320941
; APPLICANT: Young, Dallan; Wigler, Michael H.; Pasano
; Ottavio
; TITLE OF INVENTION: DNA SEQUENCES ENCODING WAS ONHCOGENE,
; POLYPEPTIDES ENCODED THEREFROM AND DIAGNOSTIC AND OTHER METHODS
; BASED THEREFROM
; NUMBER OF SEQUENCES: 2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/06/872,087
; FILING DATE: 06-JUN-1986
; SEQ ID NO:2
; LENGTH: 325
5320941-2

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```

Query Match 25.1%; Score 423.5; DB 6; Length 325;
Best Local Similarity 37.0%; Pred. No. 6.7e-30;
Matches 101; Conservative 58; Mismatches 93; Indels 21; Gaps 6;

QY 37 VSUVAITGNVAVLWLLGCRMRNAVSIYILNLVADFLSLGHIICS-----PLRLINIR 91
DB 42 ISPVGVFNGILLWFLCFRRNRPFTVYITHUSIADISLLFCIFILSDYALDYELSSGH 101
QY 92 HPISKILSPVMTFPYPIGLSMLSAISTERCLSLPDIWYHCRPRYLSSVMCVLLWALS 151
DB 102 YTVITLSVTFLFGYNTGLYLLTAISVERCLSVLYPIWYRCHRPKYQSALVCALLWALS 161
QY 152 LRSILEMPCDFLFGSADSVWCETSD-----FITI-AMLVFLCVLTCGSSLYLVYLILC 204
DB 162 LVTMEYVMCIHTEESDS-----PNDCPAVITFIALLSLFLVFTGLMLV-SSITLVVKIPK 216
QY 205 GSRKMPITRLYITLLVTLVFLVLCGLPFGIOWALFSRIHLDKVLVLFCHVLSVIFLSALN 264
DB 217 NTWASHSSKLYIVYVWIIIFLI-----FAMWELLVLYLYEYVSTFGNLDISLLFSTIN 272
QY 265 SSANPIYFVGSPFRQRQNLKVLQALQD 297
DB 273 SSANNFIYFVGSSKKRFXQLKVVYVTRAFKD 305

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```

RESULT 2
US-08-118-270-52
; Sequence 52, Application US/08118270
; Patent No. 5508384
; GENERAL INFORMATION:
; APPLICANT: Murphy, Randall B.
; APPLICANT: Schuster, David I.
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
; RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF

```

NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118,270
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY=2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 282 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-118-270-52

Query Match 23.0%; Score 388.5; DB 1; Length 282;
Best Local Similarity 34.4%; Pred. No. 7.2e-27;
Matches 96; Conservative 53; Mismatches 87; Indels 43; Gaps 7;

QY 37 VSLVALTGNVAVLW-----LLGCRMRNAVSIYIINL-VAADFLFLSG 78
Db 9 ISPGVFVENGLLWFLCFTVYTHLSADISSLFC-----IFILSDIADLYELSSG 60
QY 79 HIICSPRLNIRHPISKILSPVMTFFYIGLSMISAISTERCILSWPIWYCHRRPYL 138
Db 61 H-----YTVITLSVTFELGYNTGLYLLTAISVERCLSVLYPWYCHRRPKYQ 108
QY 139 SSMVCVILWALSLLRSILEWFCDFLFGADSVWCETSDFTITAWLVFLCVLGGSSVL 198
Db 109 SALVCALLWALSCLVTM-YVMCIDRFEESHRSNDCRAVIFIALSFLVFTSVSSTIL 167
QY 199 LVRILCGSRKMPRLTRLYVTILLTVLFLCGLPFGIQWALFSRIHLDWKVLFCHVHLVSI 258
Db 168 VVKIRKNTWASHSSKLYIVIMVTIIIFLPAMPRLLYLYEY---WST-FGNLHHISL 223
QY 259 FLSALNSANPIIYFFVGSFRQRQNLKVLORALQD 297
Db 224 LFTSTINSSANPIIYFFVGSKKKFKESLKVLTAFKQD 262

RESULT 3
PCT-US93-08528-52
Sequence 52, Application PC/TUS9308528
GENERAL INFORMATION:
APPLICANT: New York University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington

STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08528
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY=2 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 282 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US93-08528-52

Query Match 23.0%; Score 388.5; DB 5; Length 282;
Best Local Similarity 34.4%; Pred. No. 7.2e-27;
Matches 96; Conservative 53; Mismatches 87; Indels 43; Gaps 7;

QY 37 VSLVALTGNVAVLW-----LLGCRMRNAVSIYIINL-VAADFLFLSG 78
Db 9 ISPGVFVENGLLWFLCFTVYTHLSADISSLFC-----IFILSDIADLYELSSG 60
QY 79 HIICSPRLNIRHPISKILSPVMTFFYIGLSMISAISTERCILSWPIWYCHRRPYL 138
Db 61 H-----YTVITLSVTFELGYNTGLYLLTAISVERCLSVLYPWYCHRRPKYQ 108
QY 139 SSMVCVILWALSLLRSILEWFCDFLFGADSVWCETSDFTITAWLVFLCVLGGSSVL 198
Db 109 SALVCALLWALSCLVTM-YVMCIDRFEESHRSNDCRAVIFIALSFLVFTSVSSTIL 167
QY 199 LVRILCGSRKMPRLTRLYVTILLTVLFLCGLPFGIQWALFSRIHLDWKVLFCHVHLVSI 258
Db 168 VVKIRKNTWASHSSKLYIVIMVTIIIFLPAMPRLLYLYEY---WST-FGNLHHISL 223
QY 259 FLSALNSANPIIYFFVGSFRQRQNLKVLORALQD 297
Db 224 LFTSTINSSANPIIYFFVGSKKKFKESLKVLTAFKQD 262

RESULT 4
US-08-118-270-76
Sequence 76, Application US/08118270
Patent No. 5508384
GENERAL INFORMATION:
APPLICANT: Murphy, Randall B.
APPLICANT: Schuster, David I.
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004


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/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US 08/118,270
/ FILING DATE: 09-SEP-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/943,236
/ FILING DATE: 10-SEP-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Townsend, Kevin G.
/ REGISTRATION NUMBER: 34,033
/ REFERENCE/DOCKET NUMBER: MURPHY=2A
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-628-5197
/ TELEFAX: 202-737-3528
/ TELEX: 248633
/ INFORMATION FOR SEQ ID NO: 76:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 298 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: linear
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ PCT-US-08-118-270-76

Query Match 20.4%; Score 344; DB 1; Length 298;
Best Local Similarity 31.3%; Pred. No. 6.6e-23;
Matches 94; Conservative 58; Mismatches 114; Indels 34; Gaps 11;

QY 33 LTCIVSLVALTGNAVVLWLLGCRMERNVSIYI--LNLVAADFPLSGHICSPRLINI 90
Db 8 LLCLCGLV--GNGVLVWFFGFSIKRTPFSIYVFLHIASADGIYLFSAV---IALLNM 61
QY 91 RHPISKI-----LSPVMTFPFPIGLSMLSAISTERCLSIILWPIWHCRPRYLSVMCV 144
Db 62 GTFLGSPDPYVRVRSRIVGLTFFAGVSLPLPAISIERCVSVPFPMWYRRRPKRLSAGVCA 121
QY 145 LLWALSILRSILEMWFCDPLFGADSVWCETSDFTITIAWLF-----LCVVLGSSSLVLL 199
Db 122 LLWLSFLVTSIHNYFC--LLGHEASGTACLNMDISLGLILFFLFCPIWVLP-----IAL 176
QY 200 VRILGSRKMPIT--RLYVTTILTVLVLGCLPFGIQWALFSRIHLDW--KVLFCVHLV 256
Db 177 LHVECRARRQRSAKLNHVLAIVSVFLVSSYILGIDWELF-----WVFIQAPPPPEYV 230
QY 257 SIFLSALNSSANPIIYFFVGSFRQRNQLKVLQALQDTPVEDEGGWLPQE--TLEL 315
Db 231 RLDCICINSSAKPIVFIAGRDKSQRLWEPRLRVFORALRDGAEPGDAASPTNTVTNMEM 290

RESULT 5
PCT-US93-08528-76
/ Sequence 76, Application PC/TUS9308528
/ GENERAL INFORMATION:
/ APPLICANT: New York University
/ TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
/ NUMBER OF SEQUENCES: 348
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: BROWDY AND NETMARK
/ STREET: 419 Seventh Street, N.W., Suite 300
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20004
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
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/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US93/08528
/ FILING DATE: 09-SEP-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/943,236
/ FILING DATE: 10-SEP-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Townsend, Kevin G.
/ REGISTRATION NUMBER: 34,033
/ REFERENCE/DOCKET NUMBER: MURPHY=2 PCT
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-628-5197
/ TELEFAX: 202-737-3528
/ TELEX: 248633
/ INFORMATION FOR SEQ ID NO: 76:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 298 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ PCT-US93-08528-76

Query Match 20.4%; Score 344; DB 5; Length 298;
Best Local Similarity 31.3%; Pred. No. 6.6e-23;
Matches 94; Conservative 58; Mismatches 114; Indels 34; Gaps 11;

QY 33 LTCIVSLVALTGNAVVLWLLGCRMERNVSIYI--LNLVAADFPLSGHICSPRLINI 90
Db 8 LLCLCGLV--GNGVLVWFFGFSIKRTPFSIYVFLHIASADGIYLFSAV---IALLNM 61
QY 91 RHPISKI-----LSPVMTFPFPIGLSMLSAISTERCLSIILWPIWHCRPRYLSVMCV 144
Db 62 GTFLGSPDPYVRVRSRIVGLTFFAGVSLPLPAISIERCVSVPFPMWYRRRPKRLSAGVCA 121
QY 145 LLWALSILRSILEMWFCDPLFGADSVWCETSDFTITIAWLF-----LCVVLGSSSLVLL 199
Db 122 LLWLSFLVTSIHNYFC--LLGHEASGTACLNMDISLGLILFFLFCPIWVLP-----IAL 176
QY 200 VRILGSRKMPIT--RLYVTTILTVLVLGCLPFGIQWALFSRIHLDW--KVLFCVHLV 256
Db 177 LHVECRARRQRSAKLNHVLAIVSVFLVSSYILGIDWELF-----WVFIQAPPPPEYV 230
QY 257 SIFLSALNSSANPIIYFFVGSFRQRNQLKVLQALQDTPVEDEGGWLPQE--TLEL 315
Db 231 RLDCICINSSAKPIVFIAGRDKSQRLWEPRLRVFORALRDGAEPGDAASPTNTVTNMEM 290

RESULT 6
US-08-981-825-6
/ Sequence 6, Application US/08981825
/ Patent No. 6040426
/ GENERAL INFORMATION:
/ APPLICANT: OGAWA, KAZUYAUKI
/ APPLICANT: TANAKA, KINUYA
/ APPLICANT: NAGATA, KINUYA
/ APPLICANT: TAKANO, SYOICHI
/ TITLE OF INVENTION: PROTEIN SPECIFIC TO HUMAN
/ NUMBER OF SEQUENCES: 6
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Knobbe, Martens, Olson & Bear
/ STREET: 620 Newport Center Drive 16th Floor
/ CITY: Newport Beach
/ STATE: CA
/ COUNTRY: U.S.A.
/ ZIP: 92660
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq Version 1.5
/ CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/08/981,825
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: MSHIM4.001APC
; TELEPHONE: 714-760-0404
; TELEFAX: 714-760-9502
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 395 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-981-825-6

Query Match 15.1%; Score 255.5; DB 3; Length 395;
Best Local Similarity 25.9%; Pred. No. 6.2e-15;
Matches 83; Conservative 56; Mismatches 107; Indels 75; Gaps 10;

QY 36 IVSLVLTGNVAVLWLLGCMRRNAVSIYILNLVAADFL-----FLS-----G 78
Db 41 LASLGLGVNGVILFVVGCRMRTQVTTWVHLALSDLLASALPFTYFLAVGHSWELG 100
QY 79 HIICSPRLNIRHPISKILSPVMTFFYFGLSMLSAISTERCLSLIWPYHCRPRYL 138
Db 101 TTFC-----KLHSSIFFLNMFASGFLLSAISLDRCLQVVRPVAQNHTVAA 147
QY 139 SSVMCVLLWALSLLRSILEWMFCDFLPSGADSVWC-----E 174
Db 148 AHKVCVLWALAVLNTVYFVFRDTISRLDGRIMCYNNVLLNPGDPDRDATCNSRQAALA 207
QY 175 TSDFTITAWLVFLCVLWCGSLVLLVRILCGSRKMPILTRYVITLLTVLVLGCPFGI 234
Db 208 VSKPL-LAFVLPLAIASSHAASVSL-RLQHRGRRP-GRFVRLVAAVVAALCWGPYHV 264
QY 235 QWALFSPRIH-----LDWKVLFCHVHLVSIFLSAL---NSSANPILYFFVGSFRQQR 284
Db 265 FSLLEARAHANPGLRPLVWRGL-----PFVTSLAFFNSVANPVLVLTCPDMLRKL 316
QY 285 QNLKVLQALQDTPEVDEGG 305
Db 317 RSLRTVLESVLVDSDSELGGAG 337

RESULT 7
US-09-480-784-6
; Sequence 6, Application US/09480784
; Patent No. 6166186
; GENERAL INFORMATION:
; APPLICANT: OGAWA, KAZUYAUKI
; TANAKA, KAZUYA
; NAGATA, KINYA
; TAKANO, SYOICHI
; TITLE OF INVENTION: PROTEIN SPECIFIC TO HUMAN
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette

; APPLICATION NUMBER: US/08/981,825
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: MSHIM4.001APC
; TELEPHONE: 714-760-0404
; TELEFAX: 714-760-9502
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 395 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-981-825-6

Query Match 15.1%; Score 255.5; DB 3; Length 395;
Best Local Similarity 25.9%; Pred. No. 6.2e-15;
Matches 83; Conservative 56; Mismatches 107; Indels 75; Gaps 10;

QY 36 IVSLVLTGNVAVLWLLGCMRRNAVSIYILNLVAADFL-----FLS-----G 78
Db 41 LASLGLGVNGVILFVVGCRMRTQVTTWVHLALSDLLASALPFTYFLAVGHSWELG 100
QY 79 HIICSPRLNIRHPISKILSPVMTFFYFGLSMLSAISTERCLSLIWPYHCRPRYL 138
Db 101 TTFC-----KLHSSIFFLNMFASGFLLSAISLDRCLQVVRPVAQNHTVAA 147
QY 139 SSVMCVLLWALSLLRSILEWMFCDFLPSGADSVWC-----E 174
Db 148 AHKVCVLWALAVLNTVYFVFRDTISRLDGRIMCYNNVLLNPGDPDRDATCNSRQAALA 207
QY 175 TSDFTITAWLVFLCVLWCGSLVLLVRILCGSRKMPILTRYVITLLTVLVLGCPFGI 234
Db 208 VSKPL-LAFVLPLAIASSHAASVSL-RLQHRGRRP-GRFVRLVAAVVAALCWGPYHV 264
QY 235 QWALFSPRIH-----LDWKVLFCHVHLVSIFLSAL---NSSANPILYFFVGSFRQQR 284
Db 265 FSLLEARAHANPGLRPLVWRGL-----PFVTSLAFFNSVANPVLVLTCPDMLRKL 316
QY 285 QNLKVLQALQDTPEVDEGG 305
Db 317 RSLRTVLESVLVDSDSELGGAG 337

RESULT 8
US-07-759-568-2
; Sequence 2, Application US/07759568
; Patent No. 5374506
; GENERAL INFORMATION:
; APPLICANT: Murphy, Philip M.
; TITLE OF INVENTION: Cloning of cDNA Encoding a Functional
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cushman, Darby & Cushman
; STREET: 1615 L Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5601
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/759,568
FILING DATE: 19910913
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Scott, Watson T.
REGISTRATION NUMBER: 26581
REFERENCE/DOCKET NUMBER: WTS/5683/91535/WBH
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
TELEX: 6714627 cush
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 354 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-759-568-2

Query Match 14.0%; Score 235.5; DB 1; Length 354;
Best Local Similarity 28.9%; Pred. No. 3.2e-13;
Matches 94; Conservative 53; Mismatches 12; Indels 57; Gaps 16;
QY 10 TELTPINGRETEPC--YKQTLS---FTGLTCTVSVALTGNA--VVLWLLGCRMRNAVSI 63
DB 23 TQMPVE-KDVSFCLVVTQTKYVVVYVALFLLSLGSLWMLVLYSRSVTDV 81
QY 64 YILNLVAADFPLSGHICSP--RLNIRHPISKILSPVMTFFYIGLSMLSAISTERC 121
DB 82 YLLNLAMAP-APCPDHVGLRQGRDLFTPLCKVSLVKEVNFYSGILLACTISVDY 140
QY 122 LSILNPIWCHCRPYLSVMCVLWALSILERSILEWMFCDFLFGADSVNC-ETSDPIT 180
DB 141 LAIVOST-RTUTQKRHLVKFICGLWALSILSLPFFLRQVFSNNSPVCYEDLGHNT 199
QY 181 IAWLVLCVL-----CGSSVLVLRILC-GSRKXPLTRLYV-----TILLVLVF 225
DB 200 AKW-----CWVLRLPHTFGFLLVLMFLCYGFTLTLFOAHMGQKHRAMVIFAVLIF 255
QY 226 ILGHPFG-----IQWALFSRIHLDWKVLFCHVHLVIFLSALNSSANPIY 272
DB 256 LLCWLPYNLVLLADTLMTHTVITQTCQRNELDRALDATEI-----LGFHLSCLNPIY 309
QY 273 FVGSFRQQRQNR--LKLVLQAL 295
DB 310 AFIG-----QNFENGFLKMLAARGL 329

RESULT 9
US-07-759-568-1
Sequence 1, Application US/07759568
Patent No. 5374506
GENERAL INFORMATION:
APPLICANT: Murphy, Philip M.
TITLE OF INVENTION: Cloning of cDNA Encoding a Functional Human Interleukin-8 Receptor
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cushman, Darby & Cushman
STREET: 1615 L Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/759,568
FILING DATE: 19910913
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Scott, Watson T.
REGISTRATION NUMBER: 26581
REFERENCE/DOCKET NUMBER: WTS/5683/91535/WBH
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
TELEX: 6714627 cush
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-759-568-1
Query Match 13.4%; Score 226.5; DB 1; Length 355;
Best Local Similarity 26.3%; Pred. No. 2e-12;
Matches 82; Conservative 52; Mismatches 103; Indels 75; Gaps 13;
QY 19 EETPCYKQTLSTFTG-----LTCIVSLVALTGNA--VVLWLLGCRMRNAVSIYILNLVAAD 72
DB 30 DAAPCEPESLEINKYFVWIYVALVFLSLGSLWMLVLYSRVGSVTDVLLNLALAD 89
QY 73 FLF-----LSGHICSPILNIRHPISKILSPVMTFFYIGLSMLSAIS 117
DB 90 LLFALPLTWAASKVNGWIFGFLC-----KVSLLKEVNFYSGILLACIS 136
QY 118 TERCLSLNPIWYHCR---PRYLSVMCVLWALSILERSILEWMFCDFLFGADSVNC 173
DB 137 VDRYLAIV---HARTLTQKRYLVKFCISLWGLSLLLALFVLLFRRTVYSSNVSPAC 191
QY 174 -ETSDPITAWLVLCV--LCGSSVLVLRILC-GSRKXPLTRLYV-----TILLT 221
DB 192 YEDMGNNTANWMLLRILPQSPGFIVPLLMIFCYGFTLTLFOAHMGQKHRAMVIFAV 251
QY 222 VLVLGCGLPFG-----IQWALFSRIHLDWKVLFCHVHLVIFLSALNSSAN 268
DB 252 VLFLLCWLPYNLVLLADTLMTHTVITQTCQRNELDRALDATEI-----LGFHLSCLN 305
QY 269 PIYFFVG-SFR 279
DB 306 PLIYAFIGQKFR 317

RESULT 10
US-08-450-393A-8
Sequence 8, Application US/08450393A
Patent No. 5707815
GENERAL INFORMATION:
APPLICANT: Charo, Israel
APPLICANT: Coughlin, Shaun
TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto Square
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94306-2155
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,393A
; FILING DATE: May 25, 1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Cseri, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: UCAL-237/02US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5165
; TELEFAX: 415-8857-0663
; TELEX: 380816COOLEYPA
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYDROTHERMAL: NO
; US-08-450-393A-8

Query Match 13.4%; Score 226.5; DB 1; Length 355;
Best Local Similarity 26.3%; Pred. No. 2e-12;
Matches 82; Conservative 52; Mismatches 103; Indels 75; Gaps 13;

QY 19 BETPCYQTLSTFTG-----LTCIVSLVALTGNA-VVLWLLGCMRRNAVSIYILNLVAAD 72
Db 30 DAAPCEPESLEINKYFVVIIVYALVFLSLGNSLWLVILYSRVGRSVTDVYLLNLALAD 89
QY 73 FLF-----LSGHIICSPRLINIRHPISKILSPVMTFFPYFGLSMLSATS 117
Db 90 LLFALTLPWAASKVNGWIFGTFLC-----KVSLLKEVNFYSGILLACIS 136
QY 118 TERCLSILMPIWVHCR-----PRYLSSVMCVLLWALSLLRSILEMPCDFLFGADSVWC 173
Db 137 VDRYLAIV-----HATRTLQKRYLVKFCISLWGLSLLALPVLFLFRRTVYSSNVSPAC 191
QY 174 -ETSDFITIAWLFLCV--LCGSSLVLLVRILC-GSRKMPFLRLVY-----TILLT 221
Db 192 YEDGNNTANRWMLRLIPQSGFIVPLLMFCYGTLTFLFKAHGQKHRAMRVIFAV 251
QY 222 VLVLICGLPFG-----IQWALFSRIHLDKVLFCVHLVLSIFLSALNSSAN 268
Db 252 VLIFLLCWLFPYNVLLADTLMTQVIOETCERNHIDRALDATEI-----LGILHSLCN 305
QY 269 PIYFFVVG-SFR 279
Db 306 PLIYAFIGQKFR 317

RESULT 11
US-08-390-000A-5
; Sequence 5, Application US/08390000A
; Patent No. 5985583
; GENERAL INFORMATION:
; APPLICANT: Sealton, Stuart C.
; TITLE OF INVENTION: Cloning and Expression of
; TITLE OF INVENTION: Gonadotropin-Releasing Hormone Receptor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/390,000A
; FILING DATE: 17-FEB-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,972
; REFERENCE/DOCKET NUMBER: 6923-052
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIR
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-390-000A-5

Query Match 13.4%; Score 226.5; DB 2; Length 355;
Best Local Similarity 26.3%; Pred. No. 2e-12;
Matches 82; Conservative 52; Mismatches 103; Indels 75; Gaps 13;

QY 19 BETPCYQTLSTFTG-----LTCIVSLVALTGNA-VVLWLLGCMRRNAVSIYILNLVAAD 72
Db 30 DAAPCEPESLEINKYFVVIIVYALVFLSLGNSLWLVILYSRVGRSVTDVYLLNLALAD 89
QY 73 FLF-----LSGHIICSPRLINIRHPISKILSPVMTFFPYFGLSMLSATS 117
Db 90 LLFALTLPWAASKVNGWIFGTFLC-----KVSLLKEVNFYSGILLACIS 136
QY 118 TERCLSILMPIWVHCR-----PRYLSSVMCVLLWALSLLRSILEMPCDFLFGADSVWC 173
Db 137 VDRYLAIV-----HATRTLQKRYLVKFCISLWGLSLLALPVLFLFRRTVYSSNVSPAC 191
QY 174 -ETSDFITIAWLFLCV--LCGSSLVLLVRILC-GSRKMPFLRLVY-----TILLT 221
Db 192 YEDGNNTANRWMLRLIPQSGFIVPLLMFCYGTLTFLFKAHGQKHRAMRVIFAV 251
QY 222 VLVLICGLPFG-----IQWALFSRIHLDKVLFCVHLVLSIFLSALNSSAN 268
Db 252 VLIFLLCWLFPYNVLLADTLMTQVIOETCERNHIDRALDATEI-----LGILHSLCN 305
QY 269 PIYFFVVG-SFR 279
Db 306 PLIYAFIGQKFR 317

RESULT 12
US-08-446-669-8
; Sequence 8, Application US/08446669
; Patent No. 6132987
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,669
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; FILING DATE: May 25, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Neeley, Richard
; REGISTRATION NUMBER: 30,092
; REFERENCE/DOCKET NUMBER: UCAL-237/01US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5000
; TELEFAX: 415-857-0663
; TELEX: 380816COOLEYPA
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; PCT-US95-00476-8

Query Match      13.4%; Score 226.5; DB 3; Length 355;
Best Local Similarity 26.3%; Pred. No. 2e-12;
Matches 82; Conservative 52; Mismatches 103; Indels 75; Gaps 13;

QY 19 EETPCYKQTLSTFG-----LTCIVSLVALTGNA-VVIMLLGCRMRNNAVSIYILNLVAAD 72
Db 30 DAAPCEPESLEINKYFVVIYIALVFLSLGNSLVMLVILYSRVSRTDVIYLLNLALAD 89
QY 73 FLF-----LSGHIICSPRLNIRHPISKILSPVMTFFPYFGLSMLSAIS 117
Db 90 LLFALTLPWAASKVNGWIFGTFLC-----KVSSLKEVNFYSGILLACIS 136
QY 118 TERCLSIIMPWYHCHRR-----PRYLSSVMCVLLWALSILRSILEWMFCDFLFGSADSVWC 173
Db 137 VDRYLAIV-----HATRTLTKQRYLVKFCISLWGLSLLLALPVLFRRTVSSNVSPAC 191
QY 174 -ETSDPTITIAWLVFLCVV--LCGSSILVLRILC-GSRKMPLTRLV-----TILLT 221
Db 192 YEDMGNNTANWRMLRILPQSGFIVPLLMFCYGTFLRTLFKAHMGQKHRAMRVIFAV 251
QY 222 VLVLFLCGLPFG-----IQWALFSRIHLDWKVLFCHVHLVSIIFLSALNSSAN 268
Db 252 VLIFLLCWLPLYNLVLLADTLMTQVIOETCERNHIDRALDATEI-----LGILHSCLN 305
QY 269 PIYFFVVG-SFR 279
Db 306 PLIYAFIGQKFR 317

RESULT 13
PCT-US95-00476-8
; Sequence 8, Application PC/TUS9500476
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Robbins, Berliner & Carson
; STREET: 201 N. Figueroa Street, 5th Floor
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90012-2628
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00476
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
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; NAME: Berliner, Robert
; REGISTRATION NUMBER: 20,121
; REFERENCE/DOCKET NUMBER: 5555-291
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-977-1001
; TELEFAX: 310-977-1003
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; PCT-US95-00476-8

Query Match      13.4%; Score 226.5; DB 5; Length 355;
Best Local Similarity 26.3%; Pred. No. 2e-12;
Matches 82; Conservative 52; Mismatches 103; Indels 75; Gaps 13;

QY 19 EETPCYKQTLSTFG-----LTCIVSLVALTGNA-VVIMLLGCRMRNNAVSIYILNLVAAD 72
Db 30 DAAPCEPESLEINKYFVVIYIALVFLSLGNSLVMLVILYSRVSRTDVIYLLNLALAD 89
QY 73 FLF-----LSGHIICSPRLNIRHPISKILSPVMTFFPYFGLSMLSAIS 117
Db 90 LLFALTLPWAASKVNGWIFGTFLC-----KVSSLKEVNFYSGILLACIS 136
QY 118 TERCLSIIMPWYHCHRR-----PRYLSSVMCVLLWALSILRSILEWMFCDFLFGSADSVWC 173
Db 137 VDRYLAIV-----HATRTLTKQRYLVKFCISLWGLSLLLALPVLFRRTVSSNVSPAC 191
QY 174 -ETSDPTITIAWLVFLCVV--LCGSSILVLRILC-GSRKMPLTRLV-----TILLT 221
Db 192 YEDMGNNTANWRMLRILPQSGFIVPLLMFCYGTFLRTLFKAHMGQKHRAMRVIFAV 251
QY 222 VLVLFLCGLPFG-----IQWALFSRIHLDWKVLFCHVHLVSIIFLSALNSSAN 268
Db 252 VLIFLLCWLPLYNLVLLADTLMTQVIOETCERNHIDRALDATEI-----LGILHSCLN 305
QY 269 PIYFFVVG-SFR 279
Db 306 PLIYAFIGQKFR 317

RESULT 14
US-08-202-056-7
; Sequence 7, Application US/08202056
; Patent No. 5440021
; GENERAL INFORMATION:
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Hebert, Caroline
; APPLICANT: Kim, Kyung Jin
; APPLICANT: Lee, James
; TITLE OF INVENTION: Antibodies to Human IL-8 Type B Receptor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/202,056
; FILING DATE: 25-FEB-1994
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
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OM protein - protein search, using sw model

Run on: July 4, 2004, 08:45:34 ; Search time 79 Seconds
(without alignments)
1268.777 Million cell updates/sec

Title: US-09-787-879C-1

Perfect score: 1688

Sequence: 1 MDSIPVLGTETLPIINGREE.....EGGWLFOETLELSGSRLEQ 322

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Total number of hits satisfying chosen parameters: 1276540

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications AA:**
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13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1688	100.0	322	12	US-10-072-012-534
5	1688	100.0	322	14	US-10-183-116-31
6	1688	100.0	322	14	US-10-225-567A-674
7	1688	100.0	322	12	US-09-867-570-2
8	1683	99.7	322	12	US-10-072-012-530
9	1683	99.7	322	12	US-10-072-012-535
10	1683	99.7	322	12	US-10-401-397A-2
11	1683	99.7	322	15	US-10-292-798-1274
12	1683	98.5	322	12	US-10-391-074-2
13	1683	97.1	314	14	US-10-219-834-79
14	1557	92.2	302	14	US-10-237-467-10
15	1383	81.9	322	12	US-10-016-248-81

16	1383	81.9	322	12	US-10-072-012-172
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20	1383	81.9	322	14	US-10-183-116-16
21	1383	81.9	322	14	US-10-079-384-4
22	1383	81.9	322	14	US-10-017-161-1056
23	1383	81.9	322	14	US-10-240-998-4
24	1383	81.9	322	14	US-10-321-807-20
25	1383	81.9	322	14	US-10-237-467-12
26	1383	81.9	322	15	US-10-292-798-898
27	1383	81.9	1589	12	US-10-072-012-528
28	1383	81.9	1589	12	US-10-072-012-532
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35	1367	81.0	322	14	US-10-225-567A-689
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38	1361	80.6	322	15	US-10-292-798-1042
39	1313.5	77.8	323	12	US-10-072-012-178
40	1263	74.8	328	14	US-10-219-834-20
41	989.5	58.6	330	9	US-09-826-508-12
42	989.5	58.6	330	9	US-09-750-373-24
43	989.5	58.6	330	9	US-09-920-068A-4
44	989.5	58.6	330	12	US-10-343-650A-16
45	989.5	58.6	330	12	US-10-311-671-9

ALIGNMENTS

RESULT 1

US-09-995-225-20
; Sequence 20, Application US/09995225
; Publication No. US20020193584A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Chu, Zhi Liang
; APPLICANT: Dang, Huong T.
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Priddy, Cameron
; TITLE OF INVENTION: Endogenous And No. US20020193584A1-Endogenous Versions of Human
; FILE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0308
; CURRENT APPLICATION NUMBER: US/09/995,225
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: PCT/US99/23938
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/253,404
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/255,366
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/270,286
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/282,365
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/270,266
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/282,032
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,358
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,356
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/290,917
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/309,208

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; PRIOR FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. US20020193584A1el Sequence
US-09-995-225-20

Query Match      100.0%; Score 1688; DB 9; Length 322;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSTIPVLGTLPINGREETPCYKQTLSTGTLTCIVSLVALTGNVAVLWLLGCRMRNA 60
Db 1 MDSTIPVLGTLPINGREETPCYKQTLSTGTLTCIVSLVALTGNVAVLWLLGCRMRNA 60
QY 61 VSIYILNLVAADFLFLSGHIIICSPRLINIRHPISKILSPVMTFFPYFGLSMLSAISTER 120
Db 61 VSIYILNLVAADFLFLSGHIIICSPRLINIRHPISKILSPVMTFFPYFGLSMLSAISTER 120
QY 121 CLSILPWIYHCRPRYLSSVMCVLLWALSILRSILEWMFCDFLFGADSVWCETSDFIT 180
Db 121 CLSILPWIYHCRPRYLSSVMCVLLWALSILRSILEWMFCDFLFGADSVWCETSDFIT 180
QY 181 IAWLFLCVVLCGSSVLVLRILCGSRKMPPLTRYVITLLTVLVFLCGLPFGIQWALFS 240
Db 181 IAWLFLCVVLCGSSVLVLRILCGSRKMPPLTRYVITLLTVLVFLCGLPFGIQWALFS 240
QY 241 RIHLDWKVLFCHVHLVSIIFLSALNSSANPIIYFFVGSFRQRQRNKLVLQALQDTP 300
Db 241 RIHLDWKVLFCHVHLVSIIFLSALNSSANPIIYFFVGSFRQRQRNKLVLQALQDTP 300
QY 301 VDEGGWLPQETLELSGRLEQ 322
Db 301 VDEGGWLPQETLELSGRLEQ 322

RESULT 2
US-09-995-225-20
; Sequence 20, Application US/09995225
; Publication No. US20030139588A9
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Chu, Zhi Liang
; APPLICANT: Dang, Huong T.
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Pride, Cameron
; TITLE OF INVENTION: Endogenous And No. US20030139588A9-Endogenous Versions of Human C
; FILE REFERENCE: AREN-0308
; CURRENT APPLICATION NUMBER: US/09/995,225
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: PCT/US99/23938
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/253,404
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/255,366
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/270,286
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/282,365
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/270,266
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/282,032
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,358
; PRIOR FILING DATE: 2001-04-06

; PRIOR APPLICATION NUMBER: 60/282,356
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/290,917
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/309,208
; PRIOR FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. US20030139588A9el Sequence
US-09-995-225-20

Query Match      100.0%; Score 1688; DB 10; Length 322;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSTIPVLGTLPINGREETPCYKQTLSTGTLTCIVSLVALTGNVAVLWLLGCRMRNA 60
Db 1 MDSTIPVLGTLPINGREETPCYKQTLSTGTLTCIVSLVALTGNVAVLWLLGCRMRNA 60
QY 61 VSIYILNLVAADFLFLSGHIIICSPRLINIRHPISKILSPVMTFFPYFGLSMLSAISTER 120
Db 61 VSIYILNLVAADFLFLSGHIIICSPRLINIRHPISKILSPVMTFFPYFGLSMLSAISTER 120
QY 121 CLSILPWIYHCRPRYLSSVMCVLLWALSILRSILEWMFCDFLFGADSVWCETSDFIT 180
Db 121 CLSILPWIYHCRPRYLSSVMCVLLWALSILRSILEWMFCDFLFGADSVWCETSDFIT 180
QY 181 IAWLFLCVVLCGSSVLVLRILCGSRKMPPLTRYVITLLTVLVFLCGLPFGIQWALFS 240
Db 181 IAWLFLCVVLCGSSVLVLRILCGSRKMPPLTRYVITLLTVLVFLCGLPFGIQWALFS 240
QY 241 RIHLDWKVLFCHVHLVSIIFLSALNSSANPIIYFFVGSFRQRQRNKLVLQALQDTP 300
Db 241 RIHLDWKVLFCHVHLVSIIFLSALNSSANPIIYFFVGSFRQRQRNKLVLQALQDTP 300
QY 301 VDEGGWLPQETLELSGRLEQ 322
Db 301 VDEGGWLPQETLELSGRLEQ 322

RESULT 3
US-10-072-012-529
; Sequence 529, Application US/10072012
; Publication No. US20040033493A1
; GENERAL INFORMATION:
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Shinkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangoli, Esha
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Colman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Pena, Carol E. A
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Grosse, William M.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
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; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072,012
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267,459
; PRIOR FILING DATE: 2001-02-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 529
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-072-012-529

Query Match      100.0%; Score 1688; DB 12; Length 322;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSTIPVLGTETPIINGRETPCYKQTLSFTGLTCTIVSLVALTGNVAVLWLLGCRMRNA 60
Db 1 MDSTIPVLGTETPIINGRETPCYKQTLSFTGLTCTIVSLVALTGNVAVLWLLGCRMRNA 60

QY 61 VSIYILNLVAADFLLSGHIIICSPRLNIRHPISKILSPWMTFFYFGLSMLSAISTER 120
Db 61 VSIYILNLVAADFLLSGHIIICSPRLNIRHPISKILSPWMTFFYFGLSMLSAISTER 120

QY 121 CLSLMPWIYHCRPRRYLSSVMCVLLWALSLLRSILEWFCDFLPSGADSVWCETSDFIT 180
Db 121 CLSLMPWIYHCRPRRYLSSVMCVLLWALSLLRSILEWFCDFLPSGADSVWCETSDFIT 180

QY 181 IAWLVFLCVVLCGSSLLVLRILCGSRKMPPLTRLYVTILLTVLVFLLCGLPFGIQWALFS 240
Db 181 IAWLVFLCVVLCGSSLLVLRILCGSRKMPPLTRLYVTILLTVLVFLLCGLPFGIQWALFS 240

QY 241 RIHLDWKVLFCHVHLVSIPLSALNSSANPIIYFFVGSFRQRQRNQLKVLQALQDTPE 300
Db 241 RIHLDWKVLFCHVHLVSIPLSALNSSANPIIYFFVGSFRQRQRNQLKVLQALQDTPE 300

QY 301 VDEGGWLPQETLELSGSLEQ 322
Db 301 VDEGGWLPQETLELSGSLEQ 322

RESULT 4
US-10-072-012-534
; Sequence 534, Application US/10072012
; Publication No. US20040033493A1
; GENERAL INFORMATION:
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Shinkets, Richard
; APPLICANT: Li, Li

```

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; APPLICANT: Gangolli, Esha
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier, Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Colman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Pena, Carol E. A
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Grose, William M.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072,012
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,395
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267,459
; PRIOR FILING DATE: 2001-02-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 534
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-072-012-534

Query Match      100.0%; Score 1688; DB 12; Length 322;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSTIPVLGTETPIINGRETPCYKQTLSFTGLTCTIVSLVALTGNVAVLWLLGCRMRNA 60
Db 1 MDSTIPVLGTETPIINGRETPCYKQTLSFTGLTCTIVSLVALTGNVAVLWLLGCRMRNA 60

QY 61 VSIYILNLVAADFLLSGHIIICSPRLNIRHPISKILSPWMTFFYFGLSMLSAISTER 120
Db 61 VSIYILNLVAADFLLSGHIIICSPRLNIRHPISKILSPWMTFFYFGLSMLSAISTER 120

QY 121 CLSLMPWIYHCRPRRYLSSVMCVLLWALSLLRSILEWFCDFLPSGADSVWCETSDFIT 180
Db 121 CLSLMPWIYHCRPRRYLSSVMCVLLWALSLLRSILEWFCDFLPSGADSVWCETSDFIT 180

QY 181 IAWLVFLCVVLCGSSLLVLRILCGSRKMPPLTRLYVTILLTVLVFLLCGLPFGIQWALFS 240
Db 181 IAWLVFLCVVLCGSSLLVLRILCGSRKMPPLTRLYVTILLTVLVFLLCGLPFGIQWALFS 240

QY 241 RIHLDWKVLFCHVHLVSIPLSALNSSANPIIYFFVGSFRQRQRNQLKVLQALQDTPE 300
Db 241 RIHLDWKVLFCHVHLVSIPLSALNSSANPIIYFFVGSFRQRQRNQLKVLQALQDTPE 300

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QY 301 VDEGGWLPQETLESGSRLEQ 322
Db 301 VDEGGWLPQETLESGSRLEQ 322

RESULT 5
US-10-183-116-31
; Sequence 31, Application US/10183116
; Publication No. US20030092035A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David J.
; APPLICANT: Dong, Xinzhong
; APPLICANT: Zylka, Mark
; APPLICANT: Simon, Melvin
; APPLICANT: Han, Sang-kyou
; TITLE OF INVENTION: PAIN SIGNALING MOLECULES
; CURRENT APPLICATION NUMBER: US/10/183,116
; CURRENT FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: US 60/222,344
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: US 60/202,027
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 05/704,707
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/285,493
; PRIOR FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 09/849,869
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-183-116-31

Query Match 100.0%; Score 1688; DB 14; Length 322;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSTIPVLGTLPINGREETPCYKQTLSTGLTCTIVSLVALTGNVAVLWLLGCRMRNA 60
Db 1 MDSTIPVLGTLPINGREETPCYKQTLSTGLTCTIVSLVALTGNVAVLWLLGCRMRNA 60

QY 61 VSIYILNLVAADFLSLGHIICSPRLINIRHPISKILSPVMTFFPYFIGLSMLSAISTER 120
Db 61 VSIYILNLVAADFLSLGHIICSPRLINIRHPISKILSPVMTFFPYFIGLSMLSAISTER 120

QY 121 CLSILWPIWYHCRPRYLSSVMCVLLWALSLSILEWMCDFLFGADSVWCETSDFIT 180
Db 121 CLSILWPIWYHCRPRYLSSVMCVLLWALSLSILEWMCDFLFGADSVWCETSDFIT 180

QY 181 IAWLVFLCVLGGSSVLLVRLICGSRKMPILTRYVITLTVLFLCGLPFGIQWALFS 240
Db 181 IAWLVFLCVLGGSSVLLVRLICGSRKMPILTRYVITLTVLFLCGLPFGIQWALFS 240

QY 241 RIHLDWKVLFCHVHLVGFISALNSSANPIIYFVGSFRQRQNRQNLKVLQALQDTP 300
Db 241 RIHLDWKVLFCHVHLVGFISALNSSANPIIYFVGSFRQRQNRQNLKVLQALQDTP 300

QY 301 VDEGGWLPQETLESGSRLEQ 322
Db 301 VDEGGWLPQETLESGSRLEQ 322

RESULT 6
US-10-225-567A-674
; Sequence 674, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences

; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTOR
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 674
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-674

Query Match 100.0%; Score 1688; DB 14; Length 322;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSTIPVLGTLPINGREETPCYKQTLSTGLTCTIVSLVALTGNVAVLWLLGCRMRNA 60
Db 1 MDSTIPVLGTLPINGREETPCYKQTLSTGLTCTIVSLVALTGNVAVLWLLGCRMRNA 60

QY 61 VSIYILNLVAADFLSLGHIICSPRLINIRHPISKILSPVMTFFPYFIGLSMLSAISTER 120
Db 61 VSIYILNLVAADFLSLGHIICSPRLINIRHPISKILSPVMTFFPYFIGLSMLSAISTER 120

QY 121 CLSILWPIWYHCRPRYLSSVMCVLLWALSLSILEWMCDFLFGADSVWCETSDFIT 180
Db 121 CLSILWPIWYHCRPRYLSSVMCVLLWALSLSILEWMCDFLFGADSVWCETSDFIT 180

QY 181 IAWLVFLCVLGGSSVLLVRLICGSRKMPILTRYVITLTVLFLCGLPFGIQWALFS 240
Db 181 IAWLVFLCVLGGSSVLLVRLICGSRKMPILTRYVITLTVLFLCGLPFGIQWALFS 240

QY 241 RIHLDWKVLFCHVHLVGFISALNSSANPIIYFVGSFRQRQNRQNLKVLQALQDTP 300
Db 241 RIHLDWKVLFCHVHLVGFISALNSSANPIIYFVGSFRQRQNRQNLKVLQALQDTP 300

QY 301 VDEGGWLPQETLESGSRLEQ 322
Db 301 VDEGGWLPQETLESGSRLEQ 322

RESULT 7
US-09-867-570-2
; Sequence 2, Application US/09867570
; Publication No. US20040076951A1
; GENERAL INFORMATION:
; APPLICANT: Wei, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL000900-CIP
; CURRENT APPLICATION NUMBER: US/09/867,570
; CURRENT FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 09/695,045
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Human
US-09-867-570-2

Query Match 100.0%; Score 1688; DB 12; Length 337;
Best Local Similarity 100.0%; Pred. No. 5e-149;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSTIPVLGTLPINGREETPCYKQTLSTGLTCTIVSLVALTGNVAVLWLLGCRMRNA 60

Db 16 MDSTIPVLGTETLPINGREETPCYKQTLSTGLTCTIVSLVALTGNVAVLWLLGCRMRNA 75
Qy 61 VSIYILNLVAADFLFLSGHIIICSPRLINIRHPISKILSPVMTFPYFGLSMLSAISTER 120
Db 76 VSIYILNLVAADFLFLSGHIIICSPRLINIRHPISKILSPVMTFPYFGLSMLSAISTER 135
Qy 121 CLSILWPIWYHCRPRYLSSVMCVLLWALSLLRSILEWMFCDFLFGSADSVWCETSDFIT 180
Db 136 CLSILWPIWYHCRPRYLSSVMCVLLWALSLLRSILEWMFCDFLFGSADSVWCETSDFIT 195
Qy 181 IAWLVFLCVLWCGSSVLVLRILCGSRKMPITRLVYVITLLTVLVFLCGLPFGIOWALFS 240
Db 196 IAWLVFLCVLWCGSSVLVLRILCGSRKMPITRLVYVITLLTVLVFLCGLPFGIOWALFS 255
Qy 241 RIHLDWKVLFCHVHLVSIIFLSALNSSANPIIYFFVGSFRQNRQNLKLVLRALQDTPE 300
Db 256 RIHLDWKVLFCHVHLVSIIFLSALNSSANPIIYFFVGSFRQNRQNLKLVLRALQDTPE 315
Qy 301 VDEGGWLPQETLELSGSRLEQ 322
Db 316 VDEGGWLPQETLELSGSRLEQ 337

RESULT 8

US-10-072-012-530
; Sequence 530, Application US/10072012
; Publication No. US20040033493A1
; GENERAL INFORMATION:
; APPLICANT: Spyteck, Velizar
; APPLICANT: Zethusen, Bryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Shimkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangolli, Esha
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Colman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Pena, Carol E. A
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072,012
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,395
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975

; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267,459
; PRIOR FILING DATE: 2001-02-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 530
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-072-012-530

Query Match 99.7%; Score 1683; DB 12; Length 322;
Best Local Similarity 99.7%; Pred. NO. 1.4e-148;
Matches 321; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDSTIPVLGTETLPINGREETPCYKQTLSTGLTCTIVSLVALTGNVAVLWLLGCRMRNA 60
Db 1 MDSTIPVLGTETLPINGREETPCYKQTLSTGLTCTIVSLVALTGNVAVLWLLGCRMRNA 60
Qy 61 VSIYILNLVAADFLFLSGHIIICSPRLINIRHPISKILSPVMTFPYFGLSMLSAISTER 120
Db 61 VSIYILNLVAADFLFLSGHIIICSPRLINIRHPISKILSPVMTFPYFGLSMLSAISTER 120
Qy 121 CLSILWPIWYHCRPRYLSSVMCVLLWALSLLRSILEWMFCDFLFGSADSVWCETSDFIT 180
Db 121 CLSILWPIWYHCRPRYLSSVMCVLLWALSLLRSILEWMFCDFLFGSADSVWCETSDFIT 180
Qy 181 IAWLVFLCVLWCGSSVLVLRILCGSRKMPITRLVYVITLLTVLVFLCGLPFGIOWALFS 240
Db 181 IAWLVFLCVLWCGSSVLVLRILCGSRKMPITRLVYVITLLTVLVFLCGLPFGIOWALFS 240
Qy 241 RIHLDWKVLFCHVHLVSIIFLSALNSSANPIIYFFVGSFRQNRQNLKLVLRALQDTPE 300
Db 241 RIHLDWKVLFCHVHLVSIIFLSALNSSANPIIYFFVGSFRQNRQNLKLVLRALQDTPE 300
Qy 301 VDEGGWLPQETLELSGSRLEQ 322
Db 301 VDEGGWLPQETLELSGSRLEQ 322

RESULT 9
US-10-072-012-535
; Sequence 535, Application US/10072012
; Publication No. US20040033493A1
; GENERAL INFORMATION:
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spyteck, Kimberly
; APPLICANT: Zethusen, Bryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Shimkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangolli, Esha
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Colman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Pena, Carol E. A
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Grosse, William M.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072,012
; CURRENT FILING DATE: 2002-01-31

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; PRIORITY APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIORITY APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIORITY APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIORITY APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIORITY APPLICATION NUMBER: 60/265,395
; PRIOR FILING DATE: 2001-01-31
; PRIORITY APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
; PRIORITY APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIORITY APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIORITY APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-07
; PRIORITY APPLICATION NUMBER: 60/267,459
; PRIOR FILING DATE: 2001-02-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 535
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-072-012-535

Query Match          99.7%; Score 1683; DB 12; Length 322;
Best Local Similarity 99.7%; Pred. No. 1.4e-148;
Matches 321; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSTIPVLGTLPINGREETPCYKQTLSTGTCIVSLVALTGNVAVLLGCRMRNA 60
DB 1 MDSTIPVLGTLPINGREETPCYKQTLSTGTCIVSLVALTGNVAVLLGCRMRNA 60

QY 61 VSIYILNLVAADFLSLGSHIICSPRLINIRHPISKILSPVMTFFYFGLSMLSAISTER 120
DB 61 VSIYILNLVAADFLSLGSHIICSPRLINIRHPISKILSPVMTFFYFGLSMLSAISTER 120

QY 121 CLSILWPIWCHRRPRYLSSVMCVLLWALSLLRSILEWFCDFLFGADSVWCETSDFIT 180
DB 121 CLSILWPIWCHRRPRYLSSVMCVLLWALSLLRSILEWFCDFLFGADSVWCETSDFIT 180

QY 121 CLSILWPIWCHRRPRYLSSVMCVLLWALSLLRSILEWFCDFLFGADSVWCETSDFIT 180
DB 121 CLSILWPIWCHRRPRYLSSVMCVLLWALSLLRSILEWFCDFLFGADSVWCETSDFIT 180

QY 181 IAWLVFLCVVLCGSSLLVLRILCGSRKMPLETRLYVTILLTVLVFLLCGLPFGIQWALFS 240
DB 181 IAWLVFLCVVLCGSSLLVLRILCGSRKMPLETRLYVTILLTVLVFLLCGLPFGIQWALFS 240

QY 241 RIHLWDKVLFCVHLVSIIFUSALNSSANPIIYFVGSFRQRQRNQLKVLQALQDTPE 300
DB 241 RIHLWDKVLFCVHLVSIIFUSALNSSANPIIYFVGSFRQRQRNQLKVLQALQDTPE 300

QY 301 VDEGGWLPQETLELSGRLEQ 322
DB 301 VDEGGWLPQETLELSGRLEQ 322

RESULT 10
US-10-401-397A-2
; Sequence 2, Application US/10401397A
; Publication No. US20030212001A1
; GENERAL INFORMATION:
; APPLICANT: Perri, Krishna G.
; APPLICANT: Moffett, Serge
; APPLICANT: Abran, Daniel
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR PREVENTION AND TREATMENT OF ELEVATED
; TITLE OF INVENTION: INTRAOCULAR PRESSURE AND RELATED CONDITIONS
; FILE REFERENCE: 4518/1M674US1
; CURRENT APPLICATION NUMBER: US/10/401,397A
; PRIOR FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: US 60/367,513
; PRIOR FILING DATE: 2002-03-27
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; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-401-397A-2

Query Match          99.7%; Score 1683; DB 12; Length 322;
Best Local Similarity 99.7%; Pred. No. 1.4e-148;
Matches 321; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSTIPVLGTLPINGREETPCYKQTLSTGTCIVSLVALTGNVAVLLGCRMRNA 60
DB 1 MDSTIPVLGTLPINGREETPCYKQTLSTGTCIVSLVALTGNVAVLLGCRMRNA 60

QY 61 VSIYILNLVAADFLSLGSHIICSPRLINIRHPISKILSPVMTFFYFGLSMLSAISTER 120
DB 61 VSIYILNLVAADFLSLGSHIICSPRLINIRHPISKILSPVMTFFYFGLSMLSAISTER 120

QY 121 CLSILWPIWCHRRPRYLSSVMCVLLWALSLLRSILEWFCDFLFGADSVWCETSDFIT 180
DB 121 CLSILWPIWCHRRPRYLSSVMCVLLWALSLLRSILEWFCDFLFGADSVWCETSDFIT 180

QY 121 CLSILWPIWCHRRPRYLSSVMCVLLWALSLLRSILEWFCDFLFGADSVWCETSDFIT 180
DB 121 CLSILWPIWCHRRPRYLSSVMCVLLWALSLLRSILEWFCDFLFGADSVWCETSDFIT 180

QY 181 IAWLVFLCVVLCGSSLLVLRILCGSRKMPLETRLYVTILLTVLVFLLCGLPFGIQWALFS 240
DB 181 IAWLVFLCVVLCGSSLLVLRILCGSRKMPLETRLYVTILLTVLVFLLCGLPFGIQWALFS 240

QY 241 RIHLWDKVLFCVHLVSIIFUSALNSSANPIIYFVGSFRQRQRNQLKVLQALQDTPE 300
DB 241 RIHLWDKVLFCVHLVSIIFUSALNSSANPIIYFVGSFRQRQRNQLKVLQALQDTPE 300

QY 301 VDEGGWLPQETLELSGRLEQ 322
DB 301 VDEGGWLPQETLELSGRLEQ 322

RESULT 11
US-10-292-798-1274
; Sequence 1274, Application US/10292798
; Publication No. US20030235833A1
; GENERAL INFORMATION:
; APPLICANT: SUMA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 084335/166
; CURRENT APPLICATION NUMBER: US/10/292,798
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 10/017,161
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: JP 2001-246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2070
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1274
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-292-798-1274

Query Match          99.7%; Score 1683; DB 15; Length 322;
Best Local Similarity 99.7%; Pred. No. 1.4e-148;
Matches 321; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSTIPVLGTLPINGREETPCYKQTLSTGTCIVSLVALTGNVAVLLGCRMRNA 60
DB 1 MDSTIPVLGTLPINGREETPCYKQTLSTGTCIVSLVALTGNVAVLLGCRMRNA 60

QY 61 VSIYILNLVAADFLSLGSHIICSPRLINIRHPISKILSPVMTFFYFGLSMLSAISTER 120
DB 61 VSIYILNLVAADFLSLGSHIICSPRLINIRHPISKILSPVMTFFYFGLSMLSAISTER 120
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ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: dorsal root ganglia G-protein coupled receptor (GPCR)
OTHER INFORMATION: 7 (DRG7) (NT009307)
US-10-237-467-10

Query Match 92.3%; Score 1557; DB 14; Length 302;
Best Local Similarity 93.5%; Pred. No. 7.2e-137;
Matches 301; Conservative 1; Mismatches 0; Indels 20; Gaps 1;

QY 1 MDSTIPVLGTELPINGRETPCYKQTLSTGLTCTIVSLVLTGNAVWLLGCRMRNA 60
DB 1 MDSTIPVLGTELPINGREE-----ALTGNAVWLLGCRMRNA 40

QY 61 VSIYILNLVAADFLFSLGHIICSPRLINIRHPISKILSPVMTFPYFIGLSMLSAISTER 120
DB 41 VSIYILNLVAADFLFSLGHIICSPRLINIRHPISKILSPVMTFPYFIGLSMLSAISTER 100

QY 121 CLSILWPIWYHCRPRYLSSVMCVLLWALSILRSILEWMFCDFLFGADSVWCETSDFIT 180
DB 101 CLSILWPIWYHCRPRYLSSVMCVLLWALSILRSILEWMFCDFLFGADSVWCETSDFIT 160

QY 181 IAWLVFLCVVLCGSSLLVLRILCGSRKMPLTRLYVTILLTVLVFLLCGLPFGIQWALPS 240
DB 161 IAWLVFLCVVLCGSSLLVLRILCGSRKMPLTRLYVTILLTVLVFLLCGLPFGIQWALPS 220

QY 241 RIHLWDKVLFCVHLVSIIFLSALNSSANPIIYFFVGSFRQRQNLKVLQALQDTPE 300
DB 221 RIHLWDKVLFCVHLVSIIFLSALNSSANPIIYFFVGSFRQRQNLKVLQALQDTPE 280

QY 301 VDEGGWLPQETLELSGRLEQ 322
DB 281 VDEGGWLPQETLELSGRLEQ 302

Search completed: July 4, 2004, 08:51:42
Job time : 50 secs

RESULT 15
US-10-016-248-81
Sequence 81, Application US/10016248
Publication No. US20040033491A1
GENERAL INFORMATION:
APPLICANT: Alsbrook et al.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-218
CURRENT APPLICATION NUMBER: US/10/016,248
CURRENT FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: 60/254,329
PRIOR FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 60/291,037
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 60/255,648
PRIOR FILING DATE: 2000-12-14
PRIOR APPLICATION NUMBER: 60/297,173
PRIOR FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: 60/309,258
PRIOR FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: 60/326,393
PRIOR FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: 60/315,639
PRIOR FILING DATE: 2001-08-23
NUMBER OF SEQ ID NOS: 167
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 81
LENGTH: 322
TYPE: PRT
ORGANISM: Homo sapiens
US-10-016-248-81

Query Match 81.9%; Score 1383; DB 12; Length 322;
Best Local Similarity 83.5%; Pred. No. 1.3e-120;
Matches 269; Conservative 16; Mismatches 37; Indels 0; Gaps 0;

QY 1 MDSTIPVLGTELPINGRETPCYKQTLSTGLTCTIVSLVLTGNAVWLLGCRMRNA 60
DB 1 MDSTIPVLGTELPINGREE-----ALTGNAVWLLGCRMRNA 40

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 4, 2004, 08:33:34 ; Search time 26 Seconds
(without alignments)
1191.295 Million cell updates/sec

Title: US-09-787-879C-1
Perfect score: 1688
Sequence: 1 MDSTIPVLGTELTPINGREE.....EGGWLPQETLELGSRLBQ 322

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: Pir1:*
2: Pir2:*
3: Pir3:*
4: Pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	461	27.3	378	2 A39485	transforming prote
2	446.5	26.5	324	1 TVRTAS	transforming prote
3	430.5	25.5	325	1 TVHUAS	transforming prote
4	428.5	25.4	324	2 S51001	transforming prote
5	371	22.0	343	2 A38639	G protein-coupled
6	240	14.2	355	2 JQ1231	interleukin-8 rece
7	238	14.1	353	2 C42009	FMLP-related rece
8	235.5	14.0	354	2 A23669	interleukin-8 rece
9	226.5	13.4	360	2 A53611	interleukin-8 rece
10	220	13.0	358	2 A53752	interleukin-8 rece
11	219.5	13.0	369	2 A45291	somatostatin rece
12	219.5	13.0	369	2 A47995	somatostatin rece
13	217	12.9	351	2 B42009	FMLP-related rece
14	214.5	12.7	346	2 S22448	somatostatin rece
15	210.5	12.5	388	2 JN0605	somatostatin rece
16	210	12.4	473	2 JCS835	anaphylatoxin C3a
17	209.5	12.4	363	2 I57940	somatostatin rece
18	209	12.4	356	2 A2096	interleukin-8 rece
19	206	12.2	369	2 JC2083	somatostatin rece
20	205.5	12.2	355	2 A55733	G protein-coupled
21	205.5	12.2	384	2 A47249	brain-specific som
22	205	12.1	333	2 I65989	G protein-coupled
23	203.5	12.1	380	2 S36143	kappa opioid rece
24	202.5	12.0	380	2 A48227	kappa opioid rece
25	201.5	11.9	380	2 A55259	kappa opioid rece
26	201	11.9	352	2 A46520	N-formyl peptide r
27	199.5	11.8	380	2 JC2434	kappa opioid rece
28	199	11.8	369	2 B41795	somatostatin rece
29	198.5	11.8	380	2 JC2338	kappa opioid rece

complement C5a ana
G protein-coupled
somatostatin recep
interleukin-8 rece
somatostatin recep
somatostatin recep
G protein-coupled
N-formyl peptide c
tachykinin recepto
MIP-1 alpha recept
complement C5a ana
G protein-coupled
somatostatin recep
somatostatin recep
somatostatin recep
G protein-coupled

30 196.5 11.6 350 1 A37963
31 196.5 11.6 371 2 JC5498
32 196 11.6 384 2 JC4629
33 194.5 11.5 350 2 A39445
34 194 11.5 363 2 I57955
35 194 11.5 364 2 JN0763
36 193.5 11.5 375 2 JC5069
37 193 11.4 364 2 A49542
38 193 11.4 504 2 A41783
39 188 11.1 359 2 I49341
40 187.5 11.1 352 1 S27357
41 187 11.1 340 2 JC7695
42 186 11.0 391 2 A41795
43 186 11.0 391 2 C41795
44 186 11.0 391 2 A35297
45 185.5 11.0 353 2 JC2492

ALIGNMENTS

RESULT 1

A39485
transforming protein (mrg) - human
C:Species: Homo sapiens (man)
C:Date: 28-Feb-1992 #sequence_revision 17-Apr-1993 #text_change 16-Jul-1999
C:Accession: A39485
R:Monnot, C.; Weber, V.; Stinnakre, J.; Bihoreau, C.; Teutsch, B.; Corvol, P.; Clauser, M.; Endocrinol. 5, 1477-1487, 1991
A:Title: Cloning and functional characterization of a novel mas-related gene, modulation
A:Reference number: A39485; MUID:92130997; PMID:1723144
A:Accession: A39485
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-378 <NON>
A:Cross-references: GB:S78653; NID:G244209; PIDN:AAB21255.1; PID:G244210
C:Superfamily: mas transforming protein
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 27.3%; Score 461; DB 2; Length 378;
Best Local Similarity 37.9%; Pred. No. 2.9e-31;
Matches 107; Conservative 56; Mismatches 81; Indels 38; Gaps 10;

Qy 36 IVSLVATGNVVLWLLGCMRNNAVSTILNLVAADFLSLGHIICSLRLINIR---- 91
Db 84 LVSLCGVLLNGTVFLWLLCCG-ATNPYMYVILHLVAADVIYL-----CCSAVGFQVTLTY 138
Qy 92 HPI-----SKILSPWTFPPYFGLSMLSAISTERCLSLWPIWYHCRPRYLSSVMCV 144
Db 139 HGVVFFIPDPLALSP---PSPEVCCLLVAISTERCVCVLPFIWYRCHRPKYTSNVCT 195
Qy 145 LLWALSLLRSILEMFMFCDFLFGSADSVWCSTSD---FTIANL--VFLCVLGCSSILVL 199
Db 196 LINGLPPCINIVKSLFTY-----WKHVKACVIFLKLGLFHALSLVMCVSLLTL 247
Qy 200 VRILCGSRKMLPRLVYVTLTLVLVFLCGLPFGIQWALFSRIHLDKVLFCFHLVLSIF 259
Db 248 IRLCCSQQKATRVAVQISAPMELLWALPLSV-----APLITDFKFTVTSYLSLIF 302
Qy 260 LSAINSSANPIIYFFVGSFQRQRNQLKVLORALODTPEV 301
Db 303 L-IINSSANPIIYFFVGSFLRKLKESLRVILQALADKPEV 343

RESULT 2

TVRTAS
transforming protein mas - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 18-Jun-1999
C:Accession: A31816
R:Young, D.; O'Neill, K.; Jessell, T.; Wigler, M.
Proc. Natl. Acad. Sci. U.S.A. 85, 5339-5342, 1988
A:Title: Characterization of the rat mas oncogene and its high-level expression in the

A:Reference number: A31816; MUID:88276953; PMID:2455902
A:Accession: A31816
A:Molecule type: mRNA
A:Residues: 1-324 <YOU>
A:CROSS-references: GB:J03823; NID:G205313; PIDN:AAA41573.1; PID:G205314
C:Genetics:
A:Gene: mas
C:Superfamily: mas transforming protein
C:Keywords: G protein-coupled receptor; transforming protein; transmembrane protein
F:31-47/Domain: transmembrane #status predicted <TM1>
F:72-86/Domain: transmembrane #status predicted <TM2>
F:149-165/Domain: transmembrane #status predicted <TM3>
F:185-204/Domain: transmembrane #status predicted <TM4>
F:225-243/Domain: transmembrane #status predicted <TM5>
Query Match 26.5%; Score 446.5; DB 1; Length 324;
Best Local Similarity 38.0%; Pred. No. 4.1e-30;
Matches 108; Conservative 57; Mismatches 96; Indels 23; Gaps 9;
37 VSLVALTGNNAVLLGCRMRNAVSIYILNLVAADFLFSLGHIICS-----PLRLINIR 91
41 ISPLGFVENGILLWFLCFRMRNPFTVYITHLSIADISLLFCIFILSIDYALDYELSSGH 100
92 HPISKILSPVMTFFPYFGLSMLSAISTERCLSIPLWYHCRPRYLSSVMCVLLWALS 151
101 YITIVTSLVTFELFGYNTGLYLLTAISVERCLSVLPYIWRCHRPKQSAFVLCALLWALS 160
152 LRSILEWMCDFLFGSGADSVCMETSD-----FITI-AMLVFLCVLGGSSVLVLRILC 204
161 LVTTMEYVMC--IDSGEES--HSQSDCAVIFIALSFVFTPLMLV-SSTILVVKIRK 215
205 GSRKMPITRLXYTILLVFLVFLGCLPFGIQWALFSRIHLDWKVLFCHVHLVSIPLSALN 264
216 NTWASHSSKLYIVIMVTIIIFLIPAMPVRVLYLYEY---WST-FGNLHNLISLFSSTIN 271
265 SSANPIIYFFVGSFRQRNQLKVLQALQD--TPEVDEGG 306
272 SSANPIIYFFVGSKKRFSKLVLTAFKDMQPRQEGNG 315
RESULT 3
TVHUAS
transforming protein mas - human
C:Species: Homo sapiens (man)
C:Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 18-Jun-1999
C:Accession: A01375
R:Young, D.; Waechter, G.; Birchmeier, C.; Pasano, O.; Wigler, M.
Cell 45, 711-719, 1986
A:Title: Isolation and characterization of a new cellular oncogene encoding a protein with transforming activity
A:Reference number: A01375; MUID:86218084; PMID:3708691
A:Accession: A01375
A:Molecule type: DNA
A:Residues: 1-325 <YOU>
A:CROSS-references: GB:MJ3150; NID:G187388; PIDN:AAA36199.1; PID:G307158
C:Genetics:
A:Gene: GDB:MAS1
A:CROSS-references: GDB:120166; OMIM:165180
A:Map position: 6q24-6q27
C:Superfamily: mas transforming protein
C:Keywords: G protein-coupled receptor; glycoprotein; proto-oncogene; transforming protein
F:31-61/Domain: transmembrane #status predicted <TM1>
F:66-97/Domain: transmembrane #status predicted <TM2>
F:103-135/Domain: transmembrane #status predicted <TM3>
F:150-172/Domain: transmembrane #status predicted <TM4>
F:186-214/Domain: transmembrane #status predicted <TM5>
F:225-250/Domain: transmembrane #status predicted <TM6>
F:258-286/Domain: transmembrane #status predicted <TM7>
F:5,16,22,272/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 25.5%; Score 430.5; DB 1; Length 325;
Best Local Similarity 37.9%; Pred. No. 9.1e-29;
Matches 103; Conservative 56; Mismatches 94; Indels 19; Gaps 8;

37 VSLVALTGNNAVLLGCRMRNAVSIYILNLVAADFLFSLGHIICS-----PLRLINIR 91
42 ISPLGFVENGILLWFLCFRMRNPFTVYITHLSIADISLLFCIFILSIDYALDYELSSGH 101
92 HPISKILSPVMTFFPYFGLSMLSAISTERCLSIPLWYHCRPRYLSSVMCVLLWALS 151
102 YITIVTSLVTFELFGYNTGLYLLTAISVERCLSVLPYIWRCHRPKQSAFVLCALLWALS 161
152 LRSILEWMCDFLFGSGADSVCMETSD-----FITI-AMLVFLCVLGGSSVLVLRILC 205
162 LVTTMEYVMC--IDSGEES--HSQSDCAVIFIALSFVFTPLMLV-SSTILVVKIRK 217
206 SRKMPITRLXYTILLVFLVFLGCLPFGIQWALFSRIHLDWKVLFCHVHLVSIPLSALN 265
218 TWASHSSKLYIVIMVTIIIFLIPAMPVRVLYLYEY---WST-FGNLHNLISLFSSTIN 273
266 SANPIIYFFVGSFRQRNQLKVLQALQD 297
274 SANPIIYFFVGSKKRFSKLVLTAFKDMQPRQEGNG 305
RESULT 4
SS1001
transforming protein mas - mouse
N:Alternate names: mas proto-oncogene protein; probable G protein-coupled receptor mas
C:Species: Mus musculus (house mouse)
C:Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 20-Apr-2001
C:Accession: SS1001; I48647; S29619
R:Metzger, R.; Bader, M.; Ludwig, T.; Berberich, C.; Bunnemann, B.; Ganten, D.
FEBS Lett. 357, 27-32, 1995
A:Title: Expression of the mouse and rat mas proto-oncogene in the brain and peripheral
A:Reference number: SS1001; MUID:95094925; PMID:8001672
A:Accession: SS1001
A>Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-324 <MET>
A:CROSS-references: EMBL:X67735
R:Metzger, R.; Bader, M.; Ludwig, T.; Berberich, C.; Bunnemann, B.; Ganten, D.
FEBS Lett. 357, 27-32, 1995
A:Title: Expression of the mouse and rat mas proto-oncogene in the brain and peripheral
A:Reference number: I48647; MUID:95094925; PMID:8001672
A:Accession: I48647
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-87, 'I', 89-324 <RES>
A:CROSS-references: EMBL:X67735; NID:G53011; PIDN:CAA47964.1; PID:G53012
C:Genetics:
A:Gene: mas
C:Superfamily: mas transforming protein
C:Keywords: G protein-coupled receptor; proto-oncogene; transmembrane protein
Query Match 25.4%; Score 428.5; DB 2; Length 324;
Best Local Similarity 37.7%; Pred. No. 1.3e-28;
Matches 107; Conservative 56; Mismatches 98; Indels 23; Gaps 9;
37 VSLVALTGNNAVLLGCRMRNAVSIYILNLVAADFLFSLGHIICS-----PLRLINIR 91
41 ISPLGFVENGILLWFLCFRMRNPFTVYITHLSIADISLLFCIFILSIDYALDYELSSGH 100
92 HPISKILSPVMTFFPYFGLSMLSAISTERCLSIPLWYHCRPRYLSSVMCVLLWALS 151
101 YITIVTSLVTFELFGYNTGLYLLTAISVERCLSVLPYIWRCHRPKQSAFVLCALLWALS 160
152 LRSILEWMCDFLFGSGADSVCMETSD-----FITI-AMLVFLCVLGGSSVLVLRILC 204
161 LVTTMEYVMC--IDSGEES--HSQSDCAVIFIALSFVFTPLMLV-SSTILVVKIRK 215
205 GSRKMPITRLXYTILLVFLVFLGCLPFGIQWALFSRIHLDWKVLFCHVHLVSIPLSALN 264
216 NTWASHSSKLYIVIMVTIIIFLIPAMPVRVLYLYEY---WST-FGNLHNLISLFSSTIN 271
265 SSANPIIYFFVGSFRQRNQLKVLQALQD--TPEVDEGG 306

Db 181 ----AFWGDVAVLRNVFTMAKVFILHFIIGFTVPMIITVCYGIITAAKHNRHMIKS 236
QY 206 SRKMPRLTYVITLLTVLFLCGLPFP---GIQWALFSR---IHLDMKVLFCVHVLVSIF 259
Db 237 SR--PL-RVFAV---VASFFICWPFYELIGLIMAVLKEMLLNGKYKILVILNPIS-S 289
QY 260 LSAALNSANPIIYFFVGSFRQNRONKLVQLQALQDTPE 300
Db 290 LAFFNSCLNPILYVGMGRNFBRLIRSLPTSIALTEVPD 330
RESULT 8
A23669
interleukin-8 receptor, high affinity - rabbit
N/Alternate names: fMLP receptor
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 05-Nov-1999
C/Accession: A23669
R/Thomas, K.M.; Pynn, H.Y.; Navarero, J.
J/Biol. Chem. 265, 20061-20064, 1990
A/Title: Molecular cloning of the fMet-Leu-Phe receptor from neutrophils.
A/Reference number: A23669; MUID:91056034; PMID:1700779
A/Molecule type: mRNA
A/Residues: 1-354 <THO>
A/Cross-references: GB:M58021; GB:J05705; NID:g165442; PIDN:AAA31377.1; PID:g165443
C/Superfamily: vertebrate rhodopsin
C/Keywords: G protein-coupled receptor; glycoprotein; membrane protein; neutrophil
Query Match 14.0%; Score 235.5; DB 2; Length 354;
Best Local Similarity 28.9%; Pred. NO. 2.2e-12;
Matches 94; Conservative 53; Mismatches 121; Indels 57; Gaps 16;
QY 10 TELTPNGREETPC--YKOTLS---FTGLTCIVSLVALTGNA-VVLLGCGMRNNAVSI 63
Db 23 TGNPPVE-KDYSCLVVTQLNKYVVVYVALVFLSLGNSLWMLVILYSRNSRVTDV 81
QY 64 YILNLVAADFLSGHICSP---RLINIRHPISKILSPVMTFPYFIFGLSMLSAIS 121
Db 82 YILNLAMAP-AFCPDHAYLGRQKRLDFTPLCKVSVLVKEVNFYSGILLACISVDY 140
QY 122 LSLTLPWIWCHRPYLSSVMCVLLWALSILSLEWFCDFLFGADSVWC-ETSDFIT 180
Db 141 LAIVQST-RTLTKRHLVFCIGIUALSLILSLPFLFRQVFNPNSSPVCYDELGHNT 199
QY 181 IAWLFLCVL-----CGSSLLVLRILC-GSRKMPRLTYV-----TILLTVLVP 225
Db 200 AKW---CMVLRILPHTFGFILPLVWMLFCYGTLLTFLQAHGQKRAMRVIFAVLIF 255
QY 226 LLGLPFG-----IQWALFSRIHLDWKVLFCHVHLVSIPLSALNSANPIIY 272
Db 256 LLCWLPNVLLADTLMTHTVIOETCQRNELDRALDATEI-----LGFLHSCNPIIY 309
QY 273 FFVGSFRQNRON--LKLVLQAL 295
Db 310 AFIG-----QNFNGFLKMLAARGL 329
RESULT 9
A53611
interleukin-8 receptor type B - human
C/Species: Homo sapiens (man)
C/Date: 07-Oct-1994 #sequence_revision 12-Apr-1996 #text_change 05-Nov-1999
C/Accession: I37898; I37812; A53611; A39446
R/Anuja, S.K.; Shetty, A.; Tiffany, H.L.; Murphy, P.M.
J. Biol. Chem. 269, 26381-26389, 1994
A/Title: Comparison of the genomic organization and promoter function for human interleukin-8 receptor type B and human interleukin-8 receptor type A.
A/Reference number: I37898; MUID:95014476; PMID:7929358
A/Accession: I37898
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-360 <RES>
A/Cross-references: EMBL:U11869; NID:g511801; PIDN:AAB60656.1; PID:g511803

A/Accession: I38712
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-15 <RES2>
A/Cross-references: EMBL:U11872; NID:g511808; PIDN:AAA64380.1; PID:g511809; EMBL:U11873
11876; NID:g511816; PID:g511817; EMBL:U11877; NID:g511818; PID:g511819; EMBL:U11878; NI
R/Sprenger, H.; Lloyd, A.R.; Lautens, L.L.; Bonner, T.I.; Kelvin, D.J.
J. Biol. Chem. 269, 11065-11072, 1994
A/Title: Structure, genomic organization, and expression of the human interleukin-8 rec
A/Reference number: A53611; MUID:94209273; PMID:7512557
A/Accession: A53611
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 6-360 <SPR>
A/Cross-references: GB:M99412; GB:L19593
R/Murphy, P.M.; Tiffany, H.L.
Science 253, 1280-1283, 1991
A/Title: Cloning of complementary DNA encoding a functional human interleukin-8 receptc
A/Reference number: A39446; MUID:91368200; PMID:1891716
A/Accession: A39446
A/Status: preliminary; nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 6-360 <MUR>
A/Cross-references: GB:M73969
C/Comment: This receptor, unlike IL8RA, binds several peptides besides interleukin-8, i
C/Genetics:
A/Gene: GDB:IL8RB; IL8RA
A/Cross-references: GDB:127868; OMIM:146928
A/Map position: 2q35-2q35
C/Superfamily: vertebrate rhodopsin
C/Keywords: G protein-coupled receptor; transmembrane protein
Query Match 13.4%; Score 226.5; DB 2; Length 360;
Best Local Similarity 26.3%; Pred. NO. 1.3e-11;
Matches 82; Conservative 52; Mismatches 103; Indels 75; Gaps 13;
QY 19 BEPCKYQTLSPFG-----LTCIVSLVALTGNA-VVLLGCGMRNNAVSIYILNLVAAD 72
Db 35 DAAPCEPESELEINKYFVIIYALVFLSLGNSLWMLVILYSRVSRTDVLNLALAD 94
QY 73 FLF-----LSGHIICSPRLINIRHPISKILSPVMTFPYFIFGLSMLSAIS 117
Db 95 LLFALTLPWAASKVNGWIFGTLC-----KVVSLLKEVNFYSGILLACIS 141
QY 118 TERCLSLPIWVHCRR-----PRLSSVMCVLLWALSILSLEWFCDFLFGADSVWC 173
Db 142 VDRYLAIV-----HATRLTQKRYLVKFCISLWGLSLALPVLFRRTVYSSNVSPAC 196
QY 174 -ETSDFITIAWLFLCVV--LCGSSLLVLRILC-GSRKMPRLTYV-----TILLT 221
Db 197 YEDMGNTANWRMLLRILPQSGFIVFELLIMLCYGTLLTFLKAHGQKRAMRVIFAV 256
QY 222 VLVFLCGLPFG-----IQWALFSRIHLDWKVLFCHVHLVSIPLSALNSAN 268
Db 257 VLIFLLCWLPYNVLLADTLMTHTVIOETCQRNELDRALDATEI-----LGFLHSCN 310
QY 269 PIIFYFVG-SFR 279
Db 311 PLIYAFIQKFR 322
RESULT 10
A53752
interleukin-8 receptor (clone SB1a) - rabbit
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
R/Prado, G.N.; Thomas, K.M.; Suzuki, H.; LaRosa, G.J.; Wilkinson, N.; Polco, E.; Navar
J. Biol. Chem. 269, 12391-12394, 1994
A/Title: Molecular characterization of a novel rabbit interleukin-8 receptor isotype.
A/Reference number: A53752; MUID:94230294; PMID:8175642
A/Accession: A53752
A/Status: preliminary


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Query Match      12.9%; Score 217; DB 2; Length 351;  
Best Local Similarity   25.7%; Pred.No. 7.8e-11;  
Matches          88; Conservative    60; Mismatches 116; Indels     78; Gaps    18;
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Cy

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13 TPNGREETPCYKOTLSFTGLTCTVSLVAL-----TGNAVVLWTLGCRMRRAVSIV 64  
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:
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C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_change 20-Jun-2000
C:Accession: JN0605; JN0762; A47457
R:Xu, Y.; Song, J.; Bruno, J.F.; Berelowitz, M.
Biochem. Biophys. Res. Commun. 193, 648-652, 1993
A:Title: Molecular cloning and sequencing of a human somatostatin receptor, hSSTR4.
A:Reference number: JN0605; MUID:93290656; PMID:8512564
A:Accession: JN0605
A:Molecule type: DNA
A:Residues: 1-388 <XUY>
A:Cross-references: GB:L14856; NID:929499; PIDN:AAA36623.1; PID:G292500
R:Yamada, Y.; Kagimoto, S.; Kubota, A.; Yasuda, K.; Masuda, K.; Someya, Y.; Ihara, Y.; I
Biochem. Biophys. Res. Commun. 195, 844-852, 1993
A:Title: Cloning, functional expression and pharmacological characterization of a fourth
A:Reference number: JN0762; MUID:93384611; PMID:8373420
A:Accession: JN0762
A:Molecule type: DNA
A:Residues: 1-388 <YAM>
A:Cross-references: GB:D16826; NID:9693907; PIDN:BAA04106.1; PID:G693908
R:Rohrer, L.; Raulf, F.; Bruns, C.; Buettner, R.; Hofstaedter, F.; Schule, R.
Proc. Natl. Acad. Sci. U.S.A. 90, 4196-4200, 1993
A:Title: Cloning and characterization of a fourth human somatostatin receptor.
A:Reference number: A47457; MUID:93248256; PMID:8483934
A:Accession: A47457
A:Molecule type: DNA
A:Residues: 1-82, 'T', 84-364, 'K', 366-388 <ROH>
A:Cross-references: GB:L07833; NID:9307429; PIDN:AAA60565.1; PID:G307430
A:Note: sequence extracted from NCBI backbone (NCBIN:130856, NCBI:P:130858)
C:Comment: This protein mediates the diverse actions of the tetradecapeptide somatostatin.
C:Genetics:
A:Gene: GDB:SSTR4
A:Cross-references: GDB:202662; OMIM:182454
A:Map position: 20p11.2-20p11.2
A:Introns: #status absent
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; hormone receptor; lipoprotein; pho
F:47-73/Domain: transmembrane #status predicted <TM1>
F:84-109/Domain: transmembrane #status predicted <TM2>
F:121-142/Domain: transmembrane #status predicted <TM3>
F:162-184/Domain: transmembrane #status predicted <TM4>
F:208-238/Domain: transmembrane #status predicted <TM5>
F:257-284/Domain: transmembrane #status predicted <TM6>
F:291-314/Domain: transmembrane #status predicted <TM7>
F:24/Binding site: carboxylate (Asn) (covalent) #status predicted
F:119-198/Disulfide bonds: #status predicted
F:161,253/Binding site: phosphate (Ser) (covalent) (by CAMP-dependent kinase) #status pr
F:327/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match 12.5%; Score 210.5; DB 2; Length 388;
Best Local Similarity 25.9%; Pred. No. 3e-10;
Matches 94; Conservative 60; Mismatches 150; Indels 59; Gaps 14;

QY	3	STLPVLGTE-----LTPNGREET--PCYKQTLSTGLTCTI---VSLVLTG 44
Db	5	STLPQGGEEGLGTAWPASAANASSAPAEAEAVAGPDAPAAAGWVAIQCIYALVCLVGLVG 64
QY	45	NAVLLW-LLCGRNRNAVYIINLVADFLP-LSGHIICSPRLINIRH-PISKILS-- 99
Db	65	NALVIVILRYAKMKTATNYLLNLAVADELFMLSVFFVASSAAL---RHNEFGSVLCRA 121
QY	100	--PVMTPFYIGLSMLSAISTERCLSIWPYHCHRPRLYSSVMCVLLWALSILRSILE 157
Db	122	VLSVDGLNMFTSVFCLTVLSVDRYAVAVHFLRAATYRRPSVAKLINLGVWLASLLVTLPI 181
QY	158	WMFCDFL-FSGADSVNCE-----TSDFTITAMLV-----FLCVVLC-----GSSLVL 198
Db	182	AIFADTRPARGGQAVACNLQWHPHNSAVFVYVTFLLPFLVLAIGLCYLLIVKRAV 241
QY	199	LVRILCGSRMPRLRYVITLTVLVLLCGLPFGIQWALFRIHLDWKVLFCHVHLVSI 258
Db	242	ALRAGWQQRRRSEKKITRLVLMVVVFLCWMPFYV---VQLLNVAVTSLDATVNHVSL 297
QY	259	FLSALNSSANPIIYFFVSGSRQRQNLKLVLRALQDTPEVDEGGWLPQETLELSGS 318

Db 298 ILSYANSCANPILYGFLS-----DNFRSPQVLCRLCCCLGAGGAEPEPLDYAT 349
QY 319 RLE 321
Db 350 ALK 352
Search completed: July 4, 2004, 08:46:02
Job time : 27 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 4, 2004, 07:23:28 ; Search time 19 seconds
(without alignments)
882.452 Million cell updates/sec

Title: US-09-787-879C-1

Perfect score: 1688
Sequence: 1 MDSTIPVLGTELTPIINGREE.....EGGWLPOETLELSGRLEQ 322

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	461	27.3	378	1 MRG_HUMAN	P35410 homo sapien
2	446.5	26.5	324	1 MAS_RAT	P12526 rattus norv
3	430.5	25.5	325	1 MAS_HUMAN	P04201 homo sapien
4	428.5	25.4	324	1 MAS_MOUSE	P30554 mus musculus
5	409	24.2	343	1 MRGF_HUMAN	Q96ami homo sapien
6	372	22.0	343	1 MRGF_MOUSE	Q9vcj6 mus musculus
7	371	22.0	343	1 MRGF_RAT	P23749 rattus norv
8	255.5	15.1	395	1 GP44_HUMAN	Q9y5y4 homo sapien
9	246	14.6	349	1 FML2_PANTR	P79243 pan troglod
10	244	14.5	349	1 FML2_PONPY	P79237 pongo pygma
11	244	14.5	353	1 FML2_HUMAN	P25089 homo sapien
12	240	14.2	355	1 IL8A_RABIT	P21109 oryctolagus
13	239	14.2	349	1 FML2_GORGO	P79178 gorilla gor
14	236.5	14.0	382	1 GP44_MOUSE	Q92zj6 mus musculus
15	231	13.7	349	1 FML2_MACMU	P79191 macaca mula
16	228.5	13.5	345	1 CSAR_CAVPO	O70129 cavia porce
17	226.5	13.4	360	1 IL8B_HUMAN	P25025 homo sapien
18	225.5	13.4	353	1 IL8B_MACMU	Q28519 macaca mula
19	225	13.3	348	1 FML1_PONPY	P73236 pongo pygma
20	222	13.2	353	1 IL8B_GORGO	Q28422 gorilla gor
21	220	13.0	358	1 IL8B_RABIT	P25444 oryctolagus
22	219.5	13.0	353	1 IL8B_PANTR	Q28807 pan troglod
23	219.5	13.0	369	1 SSR2_MOUSE	P30875 mus musculus
24	219.5	13.0	369	1 SSR2_RAT	P30680 rattus norv
25	219	13.0	348	1 FML1_GORGO	P79177 gorilla gor
26	217	12.9	351	1 FML1_HUMAN	P25090 homo sapien
27	215	12.7	381	1 GP34_HUMAN	Q9upcs homo sapien
28	215	12.7	381	1 GP34_PANTR	P60019 pan troglod
29	212	12.6	373	1 FML1_HUMAN	Q99788 homo sapien
30	211	12.5	348	1 FML1_PANTR	P79242 pan troglod
31	211	12.5	353	1 BRB1_PIG	Q8hzn9 sus scrofa
32	211	12.5	375	1 GP34_MOUSE	Q9x1k6 mus musculus
33	210.5	12.5	388	1 SSR4_HUMAN	P31391 homo sapien

RESULT 1

MRG_HUMAN	ID	MRG_HUMAN	STANDARD;	PRT;	378 AA.
AC	P35410;				
DT	01-JUN-1994	(Rel. 29, Created)			
DT	01-JUN-1994	(Rel. 29, Last sequence update)			
DT	10-OCT-2003	(Rel. 42, Last annotation update)			
DE	Mas-related G protein-coupled receptor MRG (MAS-R) (MASL-like).				
GN	MASL OR MRG.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=92130987; PubMed=1723144;				
RA	Monnot C., Weber V., Stinnakre J., Bihoreau C., Teutsch B., Corvol P., Clauser E.;				
RT	"Cloning and functional characterization of a novel mas-related gene, modulating intracellular angiotensin II actions.";				
RL	Mol. Endocrinol. 5:1477-1487(1991).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RA	Whitaker H.;				
RL	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.				
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.				
CC	-1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors. Mas subfamily.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL;	S78653;	AAB21255.1;	--	
DR	EMBL;	AL035542;	CAB44503.1;	--	
DR	PIR;	A39485;	A39485.		
DR	Genew;	HGNC:13961;	MASL.		
DR	MIM;	607235;	--		
DR	GO;	GO:0016021;	C:integral to membrane;	NAS.	
DR	GO;	GO:0004930;	F:G-protein coupled receptor activity;	NAS	
DR	GO;	GO:0007186;	P:G-protein coupled receptor protein signalin. . . ;	NAS.	
DR	InterPro;	IPR000276;	GPCR Rhodopsin.		
DR	PRINTS;	PR00237;	GPCR RHODOPSIN.		
DR	PROSITE;	PS00237;	G PROTEIN RECEPTOR F1_1;	1.	
DR	PROSITE;	PS02622;	G PROTEIN RECEPTOR F1_2;	1.	
DR	G-protein coupled receptor; Transmembrane; Glycoprotein.				
KW	DOMAIN	1	77	EXTRACELLULAR (POTENTIAL).	
FT	TRANSMEM	78	101	1 (POTENTIAL).	
FT	DOMAIN	102	109	CYTOPLASMIC (POTENTIAL).	
FT	TRANSMEM	110	136	2 (POTENTIAL).	
FT	DOMAIN	137	154	EXTRACELLULAR (POTENTIAL).	
FT	TRANSMEM	155	169	3 (POTENTIAL).	

34	210	12.4	473	1	CSAR_RAT	O55197 rattus norv
35	209.5	12.4	363	1	SSR5_RAT	P30538 rattus norv
36	207	12.3	350	1	CSAR_RABIT	Q9tuel oryctolagus
37	207	12.3	395	1	PAR4_RAT	Q92080 rattus norv
38	206	12.2	348	1	FML1_MACMU	P79190 macaca mula
39	206	12.2	350	1	IL8A_GORGO	P55919 gorilla gor
40	206	12.2	369	1	SSR2_PIG	P34994 sus scrofa
41	205.5	12.2	349	1	IL8A_RAT	P70612 rattus norv
42	205.5	12.2	355	1	GP31_HUMAN	P46091 homo sapien
43	205.5	12.2	384	1	SSR4_RAT	P30937 rattus norv
44	205	12.1	333	1	CXCL_HUMAN	P46094 homo sapien
45	205	12.1	347	1	P2YC_HUMAN	Q9cpv9 mus musculus

ALIGNMENTS

```

FT DOMAIN 170 191 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 192 207
FT DOMAIN 208 221 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 222 248
FT TRANSMEM 249 264 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 265 286
FT TRANSMEM 287 297 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 298 317
FT TRANSMEM 318 378 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 57 57 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 378 AA; 42410 MW; 508A606294B561474 CRC64;

Query Match 27.3%; Score 461; DB 1; Length 378;
Best Local Similarity 37.9%; Pred. No. 8.5e-27;
Matches 107; Conservative 56; Mismatches 81; Indels 38; Gaps 10;

QY 36 IVSLVLTGNVAVLLGCRMRNAVSIYILNLVAADFLFLSGHIICSPRLINIR---- 91
DB 84 LVSLGVLNGTVFVLLCCG-ATNPYVYILHLVAADVYL-----CCSAGVFLQVLLTY 138

QY 92 HPI-----SKILSPVMTFFYFGLSMLSAISTERCLSLWPYWHCRPRYLSSVMCV 144
DB 139 HGVVFFIPDPLALSP----ESFEVCLCLLVAISTERCVCLFPIWYRCHRPKYTSNVCT 195

QY 145 LLWALSILRSILEMFCDFLFGADSVWCETSD---FTIAML--VFLCVLGGSLVLL 199
DB 196 LINGLPCINIVKSLFTY-----WKVKACVFLKLSGLFPHAILSLVMCVSSLTLL 247

QY 200 VRILGSRKMLPRLYVITLLTVLVLGLLPGFQIOWALFSRIHLWDKVLFCVHVLVSIF 259
DB 248 IRELCSSQQKATRVAVVQISAPMFLWALPLSV-----APLITDFKMFVITSYLISLF 302

QY 260 LSAINSSANPIIYFVGSFQORQNLKVLQALQDTEPV 301
DB 303 L-IINSSANPIIYFVGSLSRKRKLKESLRVILQALADPEV 343

RESULT 2
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ID MAS_RAT STANDARD; PRT; 324 AA.
AC P12526;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE MAS proto-oncogene.
GN MAS1 OR MAS-1 OR MAS.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=88276953; PubMed=2455902;
RA Young D., O'Neill K., Jessell T., Wigler M.;
RT "Characterization of the rat mas oncogene and its high-level expression in the hippocampus and cerebral cortex of rat brain.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:5339-5342 (1988).
CC -!- FUNCTION: Not known.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -!- CAUTION: Was originally thought to be a receptor for angiotensin II.
CC
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CC
CC EMBL; J03823; AAA4573.1; -
DR

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DR PIR; A31816; TVRTAS.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PS00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECP_F2_1; 1.
KW G-protein coupled receptor; transmembrane; Glycoprotein; Proto-oncogene.
FT DOMAIN 1 35 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 36 60 1 (POTENTIAL).
FT DOMAIN 61 64 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 65 86 2 (POTENTIAL).
FT DOMAIN 87 103 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 104 127 3 (POTENTIAL).
FT DOMAIN 128 148 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 149 171 4 (POTENTIAL).
FT DOMAIN 172 184 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 185 205 5 (POTENTIAL).
FT DOMAIN 206 223 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 224 244 6 (POTENTIAL).
FT DOMAIN 245 262 7 (POTENTIAL).
FT TRANSMEM 263 324 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 5 5 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 16 16 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 21 21 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 324 AA; 37130 MW; AD810229BF1E7D36 CRC64;

Query Match 26.5%; Score 446.5; DB 1; Length 324;
Best Local Similarity 38.0%; Pred. No. 8.4e-26;
Matches 108; Conservative 57; Mismatches 96; Indels 23; Gaps 9;

QY 37 VSLVLTGNVAVLLGCRMRNAVSIYILNLVAADFLFLSGHIICS-----PRLINIR 91
DB 41 ISPLGFVENGILLWFLCFRMRNPFTVITHLSADIALLFCIFILSDIADVDYELSSGH 100

QY 92 HPIKILSPVMTFFYFGLSMLSAISTERCLSLWPYWHCRPRYLSSVMCVLWALS 151
DB 101 YTVITLSVTFELFGYNTGLYLLTAISVERCLSVLPYWRCHRPKHOSAFVCAALWALSC 160

QY 152 LRSILEMFCDFLFGADSVWCETSD-----FTI-ANLVLGLCVLGGSLVLLVRLC 204
DB 161 LVTINWYVYC--IDSGEES--HSQSDCRVIFAILSLFVTFPLMLV-SSTILVWKIRK 215

QY 205 GSRKMLPRLYVITLLTVLVLGLLPGFQIOWALFSRIHLWDKVLFCVHVLVSIFLSALN 264
DB 216 NTWASHSSKLYIVIMVTIIIFLIFAMPNRYLLLYEY--WST-FGNLHNISLLFSTIN 271

QY 265 SSANPIIYFVGSFQORQNLKVLQALQD--TPEVDEGGG 306
DB 272 SSANPIIYFVGSKKKRFRESLKVILTRAFKDEWQPRQEGNG 315

RESULT 3
MAS_HUMAN
ID MAS_HUMAN STANDARD; PRT; 325 AA.
AC P04701;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE MAS proto-oncogene.
GN MAS1 OR MAS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=86218084; PubMed=3708691;
RA Young D., Waechter G., Birchmeier C., Fasano O., Wigler M.;
RT "Isolation and characterization of a new cellular oncogene encoding a protein with multiple potential transmembrane domains.";
RL Cell 45:711-719 (1986).

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FT TRANSMEM 104 127 3 (POTENTIAL).
FT DOMAIN 128 148 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 149 171 4 (POTENTIAL).
FT DOMAIN 172 184 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 185 205 5 (POTENTIAL).
FT DOMAIN 206 223 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 224 244 6 (POTENTIAL).
FT DOMAIN 245 262 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 263 283 7 (POTENTIAL).
FT DOMAIN 284 324 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 5 5 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 16 16 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 21 21 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 19 19 S -> I (IN REF. 2).
SQ SEQUENCE 324 AA; 36904 MW; 24F4AB729936016F CRC64;

Query Match 25.4%; Score 428.5; DB 1; Length 324;
Best Local Similarity 37.7%; Pred. No. 1.7e-24;
Matches 107; Conservative 56; Mismatches 98; Indels 23; Gaps 9;

QY 37 VSLVALTGNVAVLWLLGCRMRNAVSIYILNVAADFLFLSGHIICS-----PLRLINIR 91
Db 41 ISPLGFVENGILLWFLCFMRNRPFTVYITHLSMADISLLFCIFILSIDYALDYELSSGH 100
QY 92 HPISKILSPWTPPYFPIGLSMLSAISTERCLSIWYHCHRRPRLVSSVMCVLLWALS 151
Db 101 HYITVLSVTFPGYNTGLYLLTAISVERCLSVLYPIWYTSRPHQSAFVCAALLCASC 160
QY 152 LRSILEMWFCDLFLPSGADSVWCETSD-----FTTI-AMLVFLCVLVCGSSLLVLRILC 204
Db 161 LVITMEYVMC--IDSGES--HRSDCRAVILFIALLSLVFLVFLMLVSS--ILVVKIRK 215
QY 205 GSRKMPTRLYVTILLVFLVLCGLPFGIQWALFSLRIHLDKVLFCVHVLVSIFLSALN 264
Db 216 NTVASHSKLYIVMTVIIIFLIPAMPVRLVLYEY---WSA-FGNLHNISLLESTIN 271
QY 265 SSANPIYFFVGSFRQNRQNLKVLQALQD--TPEVDEGG 306
Db 272 SSANPIYFFVGSKKRFRSLKVLTRAFKEMQPRRGNG 315

RESULT 5
MRGF HUMAN
ID _MRGF HUMAN STANDARD; PRT; 343 AA.
AC O96AM1; OSNBKA;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Mas-related G protein-coupled receptor MRGF (Mas-related gene F protein).
DE protein).
GN MRGF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayaashi K., Ishii S.,
RA Saito K., Yamamoto J., Wakamatsu A., Nagai T., Nakamura Y.,
RA Nagahara K., Sugano S., Iwaga T.,
RT "HRI human cDNA sequencing project."
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold Z.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan M., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marudina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

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RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny K.D., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield J.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Orphan receptor. May bind to a neuropeptide and may
CC regulate nociceptor function and/or development, including the
CC sensation or modulation of pain (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC Mas subfamily.

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EMBL; AK075450; BAC11628.1; -
EMBL; BC016964; AAH16964.1; -
WIM; 607233; -
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRHOODPSN.
PROSITE; PS00237; G-PROTEIN RECEPT_F1_1; 1.
PROSITE; PS0262; G-PROTEIN RECEPT_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein.
DOMAIN 1 44 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 45 66 1 (POTENTIAL).
FT DOMAIN 67 82 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 83 104 2 (POTENTIAL).
FT DOMAIN 105 123 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 124 144 3 (POTENTIAL).
FT DOMAIN 145 160 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 161 181 4 (POTENTIAL).
FT DOMAIN 182 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 220 5 (POTENTIAL).
FT DOMAIN 221 241 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 242 263 6 (POTENTIAL).
FT DOMAIN 264 273 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 274 294 7 (POTENTIAL).
FT DOMAIN 295 343 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 4 4 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 16 16 K -> R (IN REF. 1).
SQ SEQUENCE 343 AA; 38171 MW; 168A649F5B38F154 CRC64;

Query Match 24.2%; Score 409; DB 1; Length 343;
Best Local Similarity 34.9%; Pred. No. 4.7e-23;
Matches 103; Conservative 51; Mismatches 117; Indels 24; Gaps 8;

QY 33 LTCIVSLVALTGNVAVLWLLGCRMRNAVSIYILNVAADFLFLSGHIICSPLR----- 86
Db 53 LLCLCGLV---GNGLVLPFFGFSIKRNPFSYFLHLASADVGLFSKAVFIILNTGGFLG 109
QY 87 -LINIRHPISKILSPWTPPYFPIGLSMLSAISTERCLSIWYHCHRRPRLVSSVMCVL 145
Db 110 TRADYIRSVCRVLGLCM---FLTGVSLLPAVSAERCAVIFPAMYWRPRKRLSAVVCAL 166
QY 146 LMAVLSILSILEMWFCDLFLPSGADSVWCETSD-FTTIAMLVFLCVLVCGSSLLVLRILC 204
Db 167 LMVLSLLVTLCHNYFCVFLGRGAPGACGRHMDIFLGLILLFLCCPLMVLPCIALILHVEC 226

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QY 205 GSRKMPLT-RLYVTILTLVFLVLCGLPFGIQLALPSRIHLDK--KVLFCHEVLVSIFLS 261
 Db 227 RARRQRSKLNHVLAMSVFLVSSIVLGDWFLF-----WVQIPAPPPPYVTDLCI 280
 QY 262 ALNSSANPIIYFFVGSFRQRNQNLKVLQRLQDTPVEDGGWLPQF-TLEL 315
 Db 281 CINSSAKPIVFLAGDKSQRLEWPLRWFORALRDGAELGEAGGTPNTVTNMEM 335

RESULT 6
 MRGF_MOUSE STANDARD; PRT; 343 AA.
 AC Q8VCJ6; Q912B6;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Mas-related G protein-coupled receptor MRGF (Mas-related gene F protein).
 GN MRGF.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Colon;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Vax S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ubidin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Heiton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE OF 25-343 FROM N.A.
 RC STRAIN=C57BL/6;
 RX MEDLINE=21435808; PubMed=11551509;
 RA Dong X., Han S.-K., Zylka M.J., Simon M.I., Anderson D.J.;
 RA "A diverse family of GPCRs expressed in specific subsets of
 nociceptive sensory neurons.";
 RL Cell 106:619-632(2001).
 CC -!- FUNCTION: Orphan receptor. May bind to a neuropeptide and may
 CC regulate nociceptor function and/or development, including the
 CC sensation or modulation of pain.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC Mas subfamily.
 CC
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 CC or send an email to license@sib-sib.ch).
 CC
 DR EMBL; BC019711; AAH19711.1; -
 DR EMBL; AY042211; AAK91802.1; -
 DR MGI; MGI:2384823; BC019711.

DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS; PS00237; GPCRHOOPS.
 DR PROSITE; PS00237; G-PROTEIN RECF F1_1; 1.
 DR PROSITE; PS00262; G-PROTEIN RECF F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 44
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 45 66
 FT DOMAIN 67 82
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 83 104
 FT DOMAIN 105 123
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 124 144
 FT DOMAIN 145 160
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 161 181
 FT DOMAIN 182 198
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 199 220
 FT DOMAIN 221 241
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 242 263
 FT DOMAIN 264 273
 FT TRANSMEM 274 294
 FT DOMAIN 295 343
 FT N-LINKED (GLCNAC..) (POTENTIAL).
 FT CARBOHYD 4
 SQ SEQUENCE 343 AA; 38522 MW; 358ED59587C9A317 CRC64;

Query Match 22.0%; Score 372; DB 1; Length 343;
 Best Local Similarity 33.8%; Pred. No. 2.3e-20;
 Matches 101; Conservative 53; Mismatches 113; Indels 32; Gaps 11;

QY 33 LTCIVSLVALTGNAVLMVLLGCRMRNVAIVILNVAADFLLSGHICSPRLIN--- 89
 Db 53 LLLCGLV---GNGLVJMFQFSIKTPTFSYFLHLSADGMFLSKAV---IALLNMG 106
 QY 90 -----IRHPISKILSPVMTFFYIGLSMLSAISTRCILSIWPIWYHRRPRLSSV 141
 Db 107 FLGSPDPVIR--VSRIVG-LCTF--FTGVSLPAISIERCVSVIPPTWYRRPKRLSAG 162
 QY 142 MCVLWALSLRLSILEWFMFCDFLPSGADSVNCTSDFTIAWLVFL-CVILCGSLVLV 200
 Db 163 VCALLWMLSLFVTSIHNVFCMFLGHEAPGTVCRNMDIALGILLFLFCPLVPLALIL 222
 QY 201 RILGSRKMPLT-RLYVTILTLVFLVLCGLPFGIQLALPSRIHLDK--KVLFCHEVLVS 257
 Db 223 HVECRARRQRSKLNHVLAMSVFLVSSIVLGDWFLF-----WVQIPAPPPPYV 276
 QY 258 IFLSALNSSANPIIYFFVGSFRQRNQNLKVLQRLQDTPVEDGGWLPQF-TLEL 315
 Db 277 DLICICINSSAKPIVFLAGDKSQRLEWPLRWFORALRDGAELGEAGGTPNTVTNMEM 335

RESULT 7
 MRGF_MOUSE STANDARD; PRT; 343 AA.
 AC P23749;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Mas-related G protein-coupled receptor MRGF (Mas-related gene F protein).
 GN MRGF OR RTA.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Aorta;
 RX MEDLINE=90222168; PubMed=2109324;
 RA Ross P.C., Figler R.A., Corjay M.H., Barber C.M., Adam N.,
 RA Marcus D.R., Lynch K.R.;
 RA "RTA, a candidate G protein-coupled receptor: cloning, sequencing,
 RT and tissue distribution.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:3052-3056(1990).
 CC -!- FUNCTION: Orphan receptor. May bind to a neuropeptide and may


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FT TRANSMEM 289 308 7 (POTENTIAL).
FT DOMAIN 309 395 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 4 4 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 25 25 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 104 182 POTENTIAL.
FT CONFLICT 375 395 GSCAASPTGPNALSLSTSS -> VOLRSVPADGPPPGA
FT ECHLELEPGPRRAALTRESITRVFNSISGLLPQ (IN
FT REF 1).
FT SEQUENCE 395 AA; 43239 MW; 9DBBB3B2008C1D1 CRC64;
Query Match 15.1%; Score 255.5; DB 1; Length 395;
Best Local Similarity 25.9%; Pred. No. 8.1e-12;
Matches 83; Conservative 56; Mismatches 107; Indels 75; Gaps 10;
Qy 36 IVSVALTGNVAVLWLLCGRRRAVSYIILNVADEL-----FLS-----G 78
Db 41 LASLGLVGVGVLLFVCGRRQTVVTWVHLHLSLALASLPFFTYFVAVGSHWELG 100
Qy 79 HIISPLRLNIRHPISKILSPVMTFFYFIFGLSMLSAISTERCLSIILPIWYHCRPRYL 138
Db 101 TTFC-----KLHSSIFLNMFAFGFLLSALSLDRCLQVVRPVWAQNHRTVAA 147
Qy 139 SSMVCLVWLLSLLSLELWFCDFLPSGDSVWC-----E 174
Db 148 AHKVCVLWALAVLNTVPYFVFRDTISLDRGRIMCYNNVLLNPPDRDATCNSRQAALA 207
Qy 175 TSDFTITIAWLVLCVGLCGSSLVILVRLCGSRKXPLRLVYVTLTLLVFLVLCGLPFGI 234
Db 208 VSKFL-LAFVPLAIASHAAVSL-RLQHRGRRP-GRFVRLVAVVAALCWGPHYV 264
Qy 235 QWALFSRIH-----LWKVLFCHVHLVSLFSLAL-----NSSANPIYFFVGSFRQNR 284
Db 265 FSLLEARAHANFGLRPLVWRGL-----PFVTSLAFNSVANPVLVLCPOMLRKL 316
Qy 285 ONKLVLORALQDTEVEDEGG 305
Db 317 RSLRTVLSVLVDSELGAG 337
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RESULT 9
FML2 PANTR
ID FML2 PANTR STANDARD; PRT; 349 AA.
AC P79243.
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE FMLP-related receptor II (FMLP-R-II) (Formylpeptide receptor-like 2)
DE (Fragment).
GN PPRU2.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96421539; PubMed=8824156;
RA Alvarez V., Coto B., Selen P., Gouzalek-Koccs S., Lopez-Larrea C.;
RT "Molecular evolution of the N-formyl peptide and C5a receptors in
non-human primates.";
RL Immunogenetics 44:446-452(1996).
CC -!- FUNCTION: Low affinity receptor to N-formyl-methionyl peptides,
CC which are powerful neutrophils chemotactic factors. Binding of
CC FMLP to the receptor causes activation of neutrophils. This
CC response is mediated via a G-protein that activates a
CC phosphatidylinositol-calcium second messenger system.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC ENBL; X97743; CAA66327.1; -.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; 1.
DR PROSITE; PS0282; G-PROTEIN RECEPTOR FL2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Chemotaxis.
FT DOMAIN 1 27 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 28 51 1 (POTENTIAL).
FT DOMAIN 51 60 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 62 83 2 (POTENTIAL).
FT TRANSMEM 84 100 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 101 121 3 (POTENTIAL).
FT DOMAIN 122 140 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 141 162 4 (POTENTIAL).
FT DOMAIN 163 205 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 206 226 5 (POTENTIAL).
FT DOMAIN 227 242 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 243 266 6 (POTENTIAL).
FT TRANSMEM 267 286 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 287 306 7 (POTENTIAL).
FT DOMAIN 307 >349 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 4 4 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 10 10 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 98 176 POTENTIAL.
FT NON_TER 349 349
FT SEQUENCE 349 AA; 88279872915383 CRC64;
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Query Match 14.6%; Score 246; DB 1; Length 349;
Best Local Similarity 24.3%; Pred. No. 3.6e-11;
Matches 83; Conservative 75; Mismatches 111; Indels 72; Gaps 15;
Qy 14 PINGEE-----TPCYKQTLSTFTGLTCIVSLVALTGNVAVLWLLGCRMRNAVSI 65
Db 8 PLNETEVLPEPAGHTVLMIFSLVHGVTFTGVL---GNGLVWVAGFRMTWTNTICY 64
Qy 66 LNLVAADFLSLGSHIICSPRLINI-----RHP-----ISKILSPVMTFFYFIFGLSMLSAIS 117
Db 65 LNLALADFSFA---ILPFMVSVAMREKPFSGELCKLVHVMIDINLFVSVYLITIA 120
Qy 118 TERCLSIILPIWYHCRPRYLSVMCVLLWALSLSILEWMP-----CDELFL 165
Db 121 LDRICICVLHPAAQNHRTWSLAKRVMTGLWTLTLPNFIFMTTIRTNGTTCIFNP 180
Qy 166 SGADSVKCT-----SDFITIAMLVLCVGLCGSSLVLLVRLC-----G 205
Db 181 ----AFWGDIAVERLNVFIMAKVFLILHFIIGFSMPMSIITVCYGIAAKIHNRHMK 236
Qy 206 SRKMPTRLVYVTLTLLVFLVLCGLPF---GIQWALFSR---IHLQWKLVCCHVLSIF 259
Db 237 SR--PL-RVFAAV---VASPFICWFFYELIGILMAYVLMKEMLNGYKIILVILNPTS-S 289
Qy 260 LSAINSSANPIIYFVGSFRQRONRNLKVLQALQDTP 300
Db 290 LAFNSCLNFIYVFMGRNFOERLIRSLFTSLERALTVPD 330
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RESULT 10
FML2 PONPY
ID FML2 PONPY STANDARD; PRT; 349 AA.
AC P79237.
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE FMLP-related receptor II (FMLP-R-II) (Formylpeptide receptor-like 2)
DE (Fragment).
GN PPRU2.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Pongo.
 OX NCBI_TaxID=9600;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=96421539; PubMed=8824156;
 RA Alvarez V., Coro E., Sehen F., Gouzaiek-Koces S., Lopez-Larrea C.;
 RT "Molecular evolution of the N-formyl peptide and C5a receptors in
 RT non-human primates."
 RL Immunogenetics 44:446-452(1996).
 CC -|- FUNCTION: Low affinity receptor to N-formyl-methionyl peptides,
 CC which are powerful neutrophils chemotactic factors. Binding of
 CC FMLP to the receptor causes activation of neutrophils. This
 CC response is mediated via a G-protein that activates a
 CC phosphatidylinositol-calcium second messenger system.
 CC -|- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -|- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
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 CC -----
 DR EMBL: X97741; CAA66325.1; -
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm 1; 1.
 DR PRINTS: PR00237; GPCRHOPOPSN.
 DR PROSITE: PS00237; G PROTEIN RECF F1.1; 1.
 DR PROSITE: PS0262; G PROTEIN RECF F1.2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Chemotaxis.
 FT DOMAIN 1 27 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 28 50 1 (POTENTIAL).
 FT DOMAIN 51 61 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 62 83 2 (POTENTIAL).
 FT DOMAIN 84 100 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 101 121 3 (POTENTIAL).
 FT DOMAIN 122 140 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 141 162 4 (POTENTIAL).
 FT DOMAIN 163 205 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 206 226 5 (POTENTIAL).
 FT DOMAIN 227 242 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 243 266 6 (POTENTIAL).
 FT DOMAIN 267 286 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 287 306 7 (POTENTIAL).
 FT DOMAIN 307 >349 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 4 4 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 10 10 N-LINKED (GLCNAC...) (POTENTIAL).
 FT DISULFID 98 176 POTENTIAL.
 FT NON_TER 349 349
 SQ SEQUENCE 349 AA; 39423 MW; C8298D223395EECB CRC64;
 Query Match 14.5%; Score 244; DB 1; Length 349;
 Best Local Similarity 24.2%; Pred. No. 5e-11;
 Matches 82; Conservative 74; Mismatches 115; Indels 68; Gaps 14;
 QY 14 PINGRES-----TPCYQTSLFTGLTGVISVALTGNVVLWLLGRCMRNVAISYI 65
 DB 8 PLNSESEVLPEPAGTWTWIFSLVGHVTFIFGLV---GNGLVWVAGPRTVNTVCY 64
 QY 66 LNLVAADFLFSGHICSPALINI-----RHP-----ISKILSPWTFPPYIGLSMLSAT 117
 DB 65 LNLALADFSFA---LTFPMVSVAMREKWPFGTFLCKLVHVMIDINLFVSVYLITIA 120
 QY 118 TERGLSLWPTWYHCRPRVYLSVWCVLLWALSRLRSILEWVF-----CDFLF 165
 DB 121 LDRICVLHPAKAQHRTMSLAKVMGLMTLAILVLPNFIFWTITKNGDYCIENF 190
 QY 166 SGASVWCET-----SPITIAWLVLCVLCGSSIVLVRLCG-----SR 207
 DB 181 ----PFWGDTAVESLNAPITMGKVFILHFIIGFSMPMSIITCYGIIAAKIHNNMIKS 236

QY 208 KMPLTRLYVTLLTLLVFLLCGLPF---GIQWALFSR---IHLDKVLFCHVHLVSIFLS 261
 DB 237 SSPL-RVFAAV--VASFFPICWPEYELIGILMAVLKEMLLNGKYKIILLNPTS-SLA 291
 QY 262 ALNSSANPIIYFFVGSFRQNRQNLKLVLRALQDTPE 300
 DB 292 FFNSCLNPIIYVLGNSFQBELIRSLPTSLEALTEVED 330
 RESULT 11
 FML2_HUMAN
 ID FML2_HUMAN STANDARD; PRT; 353 AA.
 AC P25089;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 15-MAR-2004 (Rel. 43, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE FMLP-related receptor II (FMLP-R-II) (Formylpeptide receptor-like 2).
 GN FPR12 OR FPR11.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92307681; PubMed=1612600;
 RA Bao L., Gerard N.P., Eddy R.L. Jr., Shows T.B., Gerard C.;
 RT "Mapping of genes for the human C5a receptor (C5AR) human FMLP
 RT receptor (FPR), and two FMLP receptor homologue orphan receptors
 RT (FPR11, FPR12) to chromosome 19."
 RL Genomics 13:437-440(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94256976; PubMed=8198572;
 RA Durstun M., Gao J.-J., Tiffany H.L., McDermott D., Murphy P.M.;
 RT "Differential expression of members of the N-formylpeptide receptor
 RT gene cluster in human phagocytes."
 RL Biochem. Biophys. Res. Commun. 201:174-179(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX Kopatz S.A., Aronstam R.S., Sharma S.V.;
 RT "cDNA clones of human proteins involved in signal transduction
 RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Shat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Villalón D.K., Wuzley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Richardson S., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Pahey J., Helton E., Kettman M., Madan A.C., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield J.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Scherch A., Schein J.E., Jones S.J.N., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
 CC -|- FUNCTION: Low affinity receptor to N-formyl-methionyl peptides,
 CC which are powerful neutrophils chemotactic factors. Binding of
 CC FMLP to the receptor causes activation of neutrophils. This
 CC response is mediated via a G-protein that activates a
 CC phosphatidylinositol-calcium second messenger system.

KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Chemotaxis.
FT DOMAIN 1 40 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 41 67 1 (POTENTIAL).
FT DOMAIN 68 73 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 74 92 2 (POTENTIAL).
FT DOMAIN 93 114 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 115 138 3 (POTENTIAL).
FT DOMAIN 139 159 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 160 184 4 (POTENTIAL).
FT DOMAIN 185 204 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 205 232 5 (POTENTIAL).
FT DOMAIN 233 247 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 248 270 6 (POTENTIAL).
FT DOMAIN 271 290 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 291 313 7 (POTENTIAL).
FT DOMAIN 314 355 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 7 7 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 21 21 BY SIMILARITY.
FT CONFLICT 115 192 DLFPALTIWAVSKGKWF ->
FT CONFLICT 90 111 PAFCDPDAVLRGRQKRLDFR (IN REF. 2).
FT CONFLICT 146 147 HA -> QS (IN REF. 2).
FT CONFLICT 204 204 R -> C (IN REF. 2).
FT CONFLICT 287 288 DI -> EL (IN REF. 2).
SQ SEQUENCE 355 AA; EPE49ACB9DIE0F21 CRC64;
Query Match 14.2%; Score 240; DB 1; Length 355;
Best Local Similarity 27.4%; Pred. No. 9.9e-11;
Matches 92; Conservative 57; Mismatches 109; Indels 78; Gaps 17;
QY 10 TELTPINGREETPC--YKQTL---FTGLTCIVSLVALTGN-VVLWLLGCMRRNAVSI 63
Db 23 TGMPEVE-KDYSPLVVTQTLNKKVYVVALVFLSLGSLVMLVILYSRNSRVTDV 81
QY 64 YILNVAADFLPSCHICSPRLIN-----TRHPISKLSLWYTFPIGLSMLSAIS 117
Db 82 YLLNVAADFLF-----ALTMPEIWAWSKEGWIFGTPLCKVSLVKEVNFYSGILLACIS 137
QY 118 TERCLSLWPIVHCR-----PRVLSVMCVLLWALSLSLSLEWFMFCDFLFGADSVWC 173
Db 138 VDRYLAIV-----HATRTLKQHLVKFICLGIWALSLSLFLFELFRQVFSNNSSPVC 192
QY 174 -ETSDFITIAWLVLCV--LQSSVLVLRILC-GSRKMPRLRV-----TILLT 221
Db 193 YEDLGHNTAKRWVRLRPHPTFTGFIPLVLMVLCYGTFLRTLPQAHMGQKRAVRVIFAV 252
QY 222 VLVPFLCGLPFGIQWALFSRHLDWKVLC-----HVHLV-----SIFLS 261
Db 253 VLIFELCWLFPNL-----VLLADTLMRTHVIGETQCRNDIDRALDATEILG 299
QY 262 ALNSANPIYFFVGSFRQNRQN--LKLVLQAL 295
Db 300 FLHSLNPIIYAFIG-----QNFNGELKMLAARGL 330
RESULT 13
FNL2_GORGO STANDARD; PRT; 349 AA.
AC P79178;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE FMLP-related receptor, II (FMLP-R-II) (Formylpeptide receptor-like 2)
DE (Fragment).
GN FPR12.
OS Gorilla gorilla gorilla (Lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX NCBI_TaxID=9595;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96421539; PubMed=8824156;

RA Alvarez V., Coto E., Sehen F., Gouzalet-Koces S., Lopez-Larrea C.;
RT "Molecular evolution of the N-formyl peptide and Csa receptors in
RL non-human primates.";
CC Immunogenetics 44:446-452(1996).
CC -!- FUNCTION: Low affinity receptor to N-formyl-methionyl peptides,
CC which are powerful neutrophils chemotactic factors. Binding of
CC FMLP to the receptor causes activation of neutrophils. This
CC response is mediated via a G-protein that activates a
CC phosphatidylinositol-calcium second messenger system.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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CC or send an email to license@isb-sib.ch).
CC EMBL: X97742; CAA66326.1; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOPOFSN.
DR PROSITE; PS00237; G-PROTEIN RECP Fl_1; 1.
DR PROSITE; PS00262; G-PROTEIN RECP Fl_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Chemotaxis.
FT DOMAIN 1 27 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 28 50 1 (POTENTIAL).
FT DOMAIN 51 61 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 62 83 2 (POTENTIAL).
FT DOMAIN 84 100 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 101 121 3 (POTENTIAL).
FT DOMAIN 122 140 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 141 162 4 (POTENTIAL).
FT DOMAIN 163 205 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 206 226 5 (POTENTIAL).
FT DOMAIN 227 242 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 243 266 6 (POTENTIAL).
FT DOMAIN 267 286 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 287 306 7 (POTENTIAL).
FT DOMAIN 307 >349 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 4 4 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 10 10 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 98 176 POTENTIAL.
FT NON_TER 349 349
SQ SEQUENCE 349 AA; 39432 MW; C6ED77CFDE023834 CRC64;
Query Match 14.2%; Score 239; DB 1; Length 349;
Best Local Similarity 25.0%; Pred. No. 1.2e-10;
Matches 85; Conservative 71; Mismatches 114; Indels 70; Gaps 15;
QY 14 PINGREE-----TPCYKOTLSFTGLTCTVSLVALTGNVVLWLLGCMRRNAVSIYI 65
Db 8 PLNETEEVLPSPAGHTVLIWIFSLLVHGVTFIFGVLF--GNGLVIVWAGFLMTRTICY 64
QY 66 LNLVAADFLF--LSGHIICSPRLINIRHP-----ISKILSPVMTFPYFGLSMLSAIST 118
Db 65 LNLALADFSFALLPFRHVSVMR---EKWFGSLCKLVHVMIDINLFVSVYLITIAL 121
QY 119 ERCLSLPFIWYHCHRRPRLYSVMCVLLWALSLSLSLEWFMF-----CDFLFS 166
Db 122 DRCICVLHPAWAQNHRMTSLAKRVMTGLWILTLPNFIPTTISTNGDYCIENF- 180
QY 167 GADSVWCET-----SDFETIAWLVLCVVLGSSVLVLRILC-----GS 206
Db 181 ----FPWGDFAVERLNVFIMTKARVILHFIIGFSPMSIIVCYGIIIAKTRHNMIKSS 237
QY 207 RKMPLTRLYVTILLVFLVLCGLPF---GIQWALFSR---IHLDMKVLFCFCHLVLSIFL 260
Db 238 R--PL-RVFAAV---VASFFICWFPEYELIGILMAVLMKEMLLNGYKIILVLIPTS-SL 290

FT	TRANSMEM	28	50	1 (POTENTIAL).
FT	DOMAIN	51	61	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	62	83	2 (POTENTIAL).
FT	DOMAIN	84	100	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	101	121	3 (POTENTIAL).
FT	DOMAIN	122	140	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	141	162	4 (POTENTIAL).
FT	DOMAIN	163	205	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	206	226	5 (POTENTIAL).
FT	DOMAIN	227	242	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	243	266	6 (POTENTIAL).
FT	DOMAIN	267	286	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	287	306	7 (POTENTIAL).
FT	DOMAIN	307	>349	CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD	4	4	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	10	10	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	DISULFID	98	176	POTENTIAL.
FT	NON_TER	349	349	
SQ	SEQUENCE	349 AA;	39531 MW;	COC92A9E5CDE250C CRC64;

Query Match 13.7%; Score 231; DB 1; Length 349;
Best Local Similarity 24.2%; Pred. No. 4.4e-10;
Matches 80; Conservative 74; Mismatches 126; Indels 50; Gaps 12;

QY	14	PINGREE-----TPCYKQILSFTGLTCIVSLVALTGNVAVLWLLGCRMRNAVSIYI	65
Db	8	PLNETEEVLPEPAGHTVLMIFSLLVHGVTFIFQVL---GNGLIVWAGFRMTRVNTICY	64
QY	66	LNLVAADFLF---LSGHIICSPRLINIRHP---ISKILSPVMTFPYFIGLSMLSAIST	118
Db	65	LNVLADFSFSAIPLPHMVSVNR---EKWFGTFLCKLVHVMIDINLFPVSVLITIAL	121
QY	119	ERCLSIILWPIWYHCRPRYLSSVNCVLLWALSRLSILEWMP-----CDFLPS	166
Db	122	DRICICVLPWAQNHRTMSLAKVMTGLWILTVLPNFIEFWTTIISTTNGDTCIFNYP	181
QY	167	-GADSVWCETSDFTITIAWLVLFCVWLCGSSLVLLVILC-----GSRKMPLTRLYVT	217
Db	182	FWGDTVVERNVFTIAKVSLLIHFIFGSIPIMSIITVCYGIIVAKIHKRWTKSRPLH	241
QY	218	ILLTVLFLCGLPF---GIQWALFSR---IHLDMKVLFCVHVLVSIPLSALNSSANPI	270
Db	242	IFTAVVASFFICWFPYELTGILMAVWLKEILLNGKYKIILVLIINPTS-SLAFFNSCLNPS	300
QY	271	IYEFVGSFRQRONKLVQLQALQDTP	300
Db	301	LYVFMGHNFOERLIRSLPTSLEALTEVPD	330

Search completed: July 4, 2004, 08:44:11
Job time : 21 secs

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OM protein - protein search, using sw model

Run on: July 4, 2004, 08:29:04 ; Search time 71 Seconds
(without alignments)
1430.942 Million cell updates/sec

Title: US-09-787-879C-1

Perfect score: 1688

Sequence: 1 MDSTIPVLGTLPINGREE.....EGGWLFPQETLGLSGRLSQ 322

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTRMBL 25: *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mhc: *
8: sp_organelle: *
9: sp_phase: *
10: sp_plant: *
11: sp_rodent: *
12: sp_virus: *
13: sp_vertebrate: *
14: sp_unclassified: *
15: sp_virus: *
16: sp_bacteriap: *
17: sp_archaeap: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1688	100.0	322	4 Q96LB0	Q96LB0 homo sapien
2	1675	99.2	322	4 Q8TDE1	Q8TDE1 homo sapien
3	1606	95.1	322	4 Q8TDE0	Q8TDE0 homo sapien
4	1411	83.6	322	4 Q8TDD9	Q8TDD9 homo sapien
5	1383	81.9	322	4 Q96LB2	Q96LB2 homo sapien
6	1382	81.9	322	4 Q8TDD7	Q8TDD7 homo sapien
7	1382	81.9	322	4 Q8TDD8	Q8TDD8 homo sapien
8	1367	81.0	322	4 Q96LA9	Q96LA9 homo sapien
9	1360	80.6	322	4 Q8TDD6	Q8TDD6 homo sapien
10	989.5	58.6	330	4 Q96LB1	Q96LB1 homo sapien
11	823.5	48.8	323	11 Q7TN42	Q7TN42 rattus norv
12	820.5	48.6	337	11 Q8R4G1	Q8R4G1 rattus norv
13	797	47.2	322	11 Q8CIF3	Q8CIF3 mus musculu
14	782	46.3	304	11 Q7TN49	Q7TN49 rattus norv
15	778	46.1	331	11 Q91YB7	Q91YB7 rattus norv
16	762	45.1	338	11 Q91ZC2	Q91ZC2 mus musculu

Q8CDY4 mus musculu
Q91WV5 mus musculu
Q7TN48 rattus norv
Q91ZC6 mus musculu
Q91WV3 mus musculu
Q91ZC5 mus musculu
Q91ZC0 mus musculu
Q91ZC3 mus musculu
Q91WV2 mus musculu
Q7TN45 rattus norv
Q91WV4 mus musculu
Q91ZC7 mus musculu
Q91ZB9 mus musculu
Q91ZC4 mus musculu
Q7TN47 rattus norv
Q7TN44 rattus norv
Q91ZC1 mus musculu
Q7TN50 rattus norv
Q7TN43 rattus norv
Q7TN46 rattus norv
Q7TN51 mus musculu
Q8TDS7 homo sapien
Q8NGK7 homo sapien
Q91ZB7 mus musculu
Q91ZB8 mus musculu
Q7TN41 rattus norv
Q7TN40 rattus norv
Q8BH18 mus musculu
Q8D5Q2 mus musculu

ALIGNMENTS

RESULT 1

Q96LB0 PRELIMINARY; PRT; 322 AA.
ID Q96LB0
AC Q96LB0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE G protein-coupled receptor.
GN MRG33.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21435808; PubMed=11551509;
RA Dong X., Han S.-K., Zyika M.J., Simon M.I., Anderson D.J.;
RT "A Diverse Family of GPCRs Expressed in Specific Subsets of
RT Nociceptive Somatosensory Neurons."
RL Cell 106:619-632(2001).
DR EMBL; AY042215; AAK91806.1; --
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR InterPro; IPR0007186; P:G-protein coupled receptor protein signalin...; IEA.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODOPGN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 322 AA; 36484 MW; 253B1BEF0CB4EB74 CRC64;

Query Match 100.0%; Score 1688; DB 4; Length 322;

Best Local Similarity 100.0%; Pred. No. 2e-141;

Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSTIPVLGTLPINGREETPCYKQTLSTGLTCTIVSLVLTGNVLTGNVLTGLTCRMRNA 60

Db 1 MDSTIPVLGTELTPIINGREETPCYKQTLSTGTCTCVSLVALTGNVAVLWLLGCMRRNA 60
QY 61 VSIYILNLVAADFLFSLGHIICSPRLINIRHPISKILSPVMTFFYFGLSMLSAISTER 120
Db 61 VSIYILNLVAADFLFSLGHIICSPRLINIRHPISKILSPVMTFFYFGLSMLSAISTER 120
QY 121 CLSILNPIWYHCRPRYLSSVMCVLLWALSLLRSILEWMFCDFLFGSADSVWCETSDFIT 180
Db 121 CLSILNPIWYHCRPRYLSSVMCVLLWALSLLRSILEWMFCDFLFGSADSVWCETSDFIT 180
QY 181 IAWLVFLCVLGGSSVLVRLICGSRKMPLTLYVTILLTVLVLFCGLPFGIQWALFS 240
Db 181 IAWLVFLCVLGGSSVLVRLICGSRKMPLTLYVTILLTVLVLFCGLPFGIQWALFS 240
QY 241 RIHLDKVLFCHVHLVSIIFLSALNSSANPIIYFFVGSFRQRQNLKVLQALQDTP 300
Db 241 RIHLDKVLFCHVHLVSIIFLSALNSSANPIIYFFVGSFRQRQNLKVLQALQDTP 300
QY 301 VDEGGWLPQETLELSGRLEQ 322
Db 301 VDEGGWLPQETLELSGRLEQ 322

RESULT 2
Q8TDE1
ID Q8TDE1 PRELIMINARY; PRT; 322 AA.
AC Q8TDE1
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DE G protein-coupled receptor SNSR1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21853733; PubMed=11850634;
RA Lembo P.M., Grazzini E., Groblewski T., O'Donnell D., Roy M.-O.,
Zhang J., Hoffert C., Cao J., Schmidt R., Pelletier M., Labarre M.,
Gosselin M., Fortin Y., Banville D., Shen S., Strom P., Payza K.,
Dray A., Walker P., Ahmad S.;
RT "Proenkephalin A gene products activate a new family of sensory
neuron-specific GPCRs.";
RL Nat. Neurosci. 5:201-209(2002).
DR EMBL; AF474987; AAL86878.2; -.
KW Receptor.
SQ SEQUENCE 322 AA; 36465 MW; 6462C5044F91EA50 CRC64;

Query Match 99.2%; Score 1675; DB 4; Length 322;
Best Local Similarity 99.1%; Pred. No. 2.8e-140;
Matches 319; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDSTIPVLGTELTPIINGREETPCYKQTLSTFTGLTCIVSLVALTGNVAVLWLLGCMRRNA 60
Db 1 MDPTIPVLGTELTPIINGREETPCYKQTLSTFTGLTCIVSLVALTGNVAVLWLLGCMRRNA 60
QY 61 VSIYILNLVAADFLFSLGHIICSPRLINIRHPISKILSPVMTFFYFGLSMLSAISTER 120
Db 61 VSIYILNLVAADFLFSLGHIICSPRLINIRHPISKILSPVMTFFYFGLSMLSAISTER 120
QY 121 CLSILNPIWYHCRPRYLSSVMCVLLWALSLLRSILEWMFCDFLFGSADSVWCETSDFIT 180
Db 121 CLSILNPIWYHCRPRYLSSVMCVLLWALSLLRSILEWMFCDFLFGSADSVWCETSDFIT 180
QY 181 IAWLVFLCVLGGSSVLVRLICGSRKMPLTLYVTILLTVLVLFCGLPFGIQWALFS 240
Db 181 IAWLVFLCVLGGSSVLVRLICGSRKMPLTLYVTILLTVLVLFCGLPFGIQWALFS 240
QY 241 RIHLDKVLFCHVHLVSIIFLSALNSSANPIIYFFVGSFRQRQNLKVLQALQDTP 300
Db 241 RIHLDKVLFCHVHLVSIIFLSALNSSANPIIYFFVGSFRQRQNLKVLQALQDTP 300

QY 301 VDEGGWLPQETLELSGRLEQ 322
Db 301 VDEGGWLPQETLELSGRLEQ 322

RESULT 3
Q8TDE0
ID Q8TDE0 PRELIMINARY; PRT; 322 AA.
AC Q8TDE0
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE G protein-coupled receptor SNSR2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21853733; PubMed=11850634;
RA Lembo P.M., Grazzini E., Groblewski T., O'Donnell D., Roy M.-O.,
Zhang J., Hoffert C., Cao J., Schmidt R., Pelletier M., Labarre M.,
Gosselin M., Fortin Y., Banville D., Shen S., Strom P., Payza K.,
Dray A., Walker P., Ahmad S.;
RT "Proenkephalin A gene products activate a new family of sensory
neuron-specific GPCRs.";
RL Nat. Neurosci. 5:201-209(2002).
DR EMBL; AF474988; AAL86879.2; -.
KW Receptor.
SQ SEQUENCE 322 AA; 36594 MW; D8C24308E3B4611B CRC64;

Query Match 95.1%; Score 1606; DB 4; Length 322;
Best Local Similarity 96.0%; Pred. No. 3.6e-134;
Matches 309; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 1 MDSTIPVLGTELTPIINGREETPCYKQTLSTFTGLTCIVSLVALTGNVAVLWLLGCMRRNA 60
Db 1 MDPTIPVLGTELTPIINGREETPCYKQTLSTFTGLTCIVSLVALTGNVAVLWLLGCMRRNA 60
QY 61 VSIYILNLVAADFLFSLGHIICSPRLINIRHPISKILSPVMTFFYFGLSMLSAISTER 120
Db 61 VSIYILNLVAADFLFSLGHIICSPRLINIRHPISKILSPVMTFFYFGLSMLSAISTER 120
QY 121 CLSILNPIWYHCRPRYLSSVMCVLLWALSLLRSILEWMFCDFLFGSADSVWCETSDFIT 180
Db 121 CLSILNPIWYHCRPRYLSSVMCVLLWALSLLRSILEWMFCDFLFGSADSVWCETSDFIT 180
QY 181 IAWLVFLCVLGGSSVLVRLICGSRKMPLTLYVTILLTVLVLFCGLPFGIQWALFS 240
Db 181 IAWLVFLCVLGGSSVLVRLICGSRKMPLTLYVTILLTVLVLFCGLPFGIQWALFS 240
QY 241 RIHLDKVLFCHVHLVSIIFLSALNSSANPIIYFFVGSFRQRQNLKVLQALQDTP 300
Db 241 RIHLDKVLFCHVHLVSIIFLSALNSSANPIIYFFVGSFRQRQNLKVLQALQDTP 300
QY 301 VDEGGWLPQETLELSGRLEQ 322
Db 301 VDEGGWLPQETLELSGRLEQ 322

RESULT 4
Q8TDD9
ID Q8TDD9 PRELIMINARY; PRT; 322 AA.
AC Q8TDD9
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DE G protein-coupled receptor SNSR3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE=21853733; PubMed=11850634;
RA Lembo P.M., Grazzini E., Groblewski T., O'Donnell D., Roy M.-O.,
RA Zhang J., Hoffert C., Cao J., Schmidt R., Pelletier M., Labarre M.,
RA Gosselin M., Fortin Y., Barville D., Shen S., Strom P., Payza K.,
RA Dray A., Walker P., Ahmad S.;
RA "Proenkephalin A gene products activate a new family of sensory
RT neuron-specific GPCRs.";
RL Nat. Neurosci. 5:201-209(2002).
DR EMBL; AF474989; AAL86880.2; -.
KW Receptor.
SQ SEQUENCE 322 AA; 36287 MW; 4C43E33E52DCBFF5 CRC64;

Query Match      83.6%; Score 1411; DB 4; Length 322;
Best Local Similarity 84.5%; Pred. No. 6,6e-117;
Matches 272; Conservative 16; Mismatches 34; Indels 0; Gaps 0;

QY 1 MDSTIPVLGTLPNGRETPCYQTLSFTGLTCIVSLVALTGNVAVLLGCRMRNA 60
Db 1 MDPTVSTLDTLTPNGTEETLCYKQTLSTLVTLCIVSLVLTGNVAVLLGCRMRNA 60

QY 61 VSIYILNVAADFLFSGHIIICSPRLINIRHPISKILSPVMTFFPIGLSMLSAISTER 120
Db 61 FSIYILNVAADFLFSGRLIYSLFSIPHTISKILYPMWFSYFAGLSFLSAVSTER 120

QY 121 CLSLWPIWYHCRPRYLSVMCVLLWALSRLSILEWMCDFLFGADSVWCSTSDFIT 180
Db 121 CLSLWPIWYHCRPRYLSVMCVLLWALSRLSILEWMCDFLFGADSVWCSTSDFIT 180

QY 181 IAWLFLCVVLCGSSVLLVRLTLCGRKXPLTRLVVTTILLTVLFLCGLPFIQWALFS 240
Db 181 VAWLFLCVVLCGSSVLLVRLTLCGRKXPLTRLVVTTILLTVLFLCGLPFIQWALFS 240

QY 241 RIHLDMKVLFCVHLVSIPLSALNSANPIIYFFVGSFRQRNQNLKVLQALQDTPPE 300
Db 241 RIHLDMKVLFCVHLVSIPLSALNSANPIIYFFVGSFRQRNQNLKVLQALQDTPPE 300

QY 301 VDEGGGWLPOETLELSGSRLEQ 322
Db 301 VDEGGGWLPOETLELSGSRLEQ 322

RESULT 5
Q96LB2 ID Q96LB2 PRELIMINARY; PRT; 322 AA.
AC Q96LB2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE G protein-coupled receptor (Seven transmembrane helix receptor).
GN MRGXI OR GPCR
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE=21435808; PubMed=11551509;
RA Dong X., Han S.-K., Zylka M.J., Simon M.I., Anderson D.J.;
RA "A Diverse Family of GPCRs Expressed in Specific Subsets of
RT Nociceptive Somatosensory Neurons.";
RL Cell 106:619-632(2001).
[2]
RN SEQUENCE FROM N.A.
RX Takeda S., Kadowaki S., Haga T., Takasasu H., Mitaku S.;
RA "Identification of G protein-coupled receptor genes from the human
RT genome sequence.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
[3]
RN SEQUENCE FROM N.A.
RX Suwa M., Sato T., Okouchi I., Azita M., Furami K., Matsumoto S.,
RA Tautumi S., Aburatani H., Asai K., Akiyama Y.;
RT "Genome-wide discovery and analysis of human seven transmembrane helix
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RT receptor genes.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AX042213; AAK91804.1; -.
DR EMBL; AB083628; BAB89341.1; -.
DR EMBL; AB065846; BAC06064.1; -.
DR GO:0016021; C:integral to membrane; IEA.
DR GO:0004872; F:receptor activity; IEA.
DR GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL_1; 1.
DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL_2; 1.
KW Receptor; Transmembrane.
SQ SEQUENCE 322 AA; 36250 MW; C7F3A9F4418E8AD1 CRC64;

Query Match      81.9%; Score 1383; DB 4; Length 322;
Best Local Similarity 83.5%; Pred. No. 2e-114;
Matches 269; Conservative 16; Mismatches 37; Indels 0; Gaps 0;

QY 1 MDSTIPVLGTLPNGRETPCYKOTLSFTGLTCIVSLVALTGNVAVLLGCRMRNA 60
Db 1 MDPTISTLDTLTPNGTEETLCYKQTLSTLVTLCIVSLVLTGNVAVLLGCRMRNA 60

QY 61 VSIYILNVAADFLFSGHIIICSPRLINIRHPISKILSPVMTFFPIGLSMLSAISTER 120
Db 61 FSIYILNVAADFLFSGRLIYSLFSIPHTISKILYPMWFSYFAGLSFLSAVSTER 120

QY 121 CLSLWPIWYHCRPRYLSVMCVLLWALSRLSILEWMCDFLFGADSVWCSTSDFIT 180
Db 121 CLSLWPIWYHCRPRYLSVMCVLLWALSRLSILEWMCDFLFGADSVWCSTSDFIT 180

QY 181 IAWLFLCVVLCGSSVLLVRLTLCGRKXPLTRLVVTTILLTVLFLCGLPFIQWALFS 240
Db 181 VAWLFLCVVLCGSSVLLVRLTLCGRKXPLTRLVVTTILLTVLFLCGLPFIQWALFS 240

QY 241 RIHLDMKVLFCVHLVSIPLSALNSANPIIYFFVGSFRQRNQNLKVLQALQDTPPE 300
Db 241 RIHLDMKVLFCVHLVSIPLSALNSANPIIYFFVGSFRQRNQNLKVLQALQDTPPE 300

QY 301 VDEGGGWLPOETLELSGSRLEQ 322
Db 301 VDEGGGWLPOETLELSGSRLEQ 322

RESULT 6
Q8TDD7 ID Q8TDD7 PRELIMINARY; PRT; 322 AA.
AC Q8TDD7;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE G protein-coupled receptor SNRS5.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE=21853733; PubMed=11850634;
RA Lembo P.M., Grazzini E., Groblewski T., O'Donnell D., Roy M.-O.,
RA Zhang J., Hoffert C., Cao J., Schmidt R., Pelletier M., Labarre M.,
RA Gosselin M., Fortin Y., Barville D., Shen S., Strom P., Payza K.,
RA Dray A., Walker P., Ahmad S.;
RA "Proenkephalin A gene products activate a new family of sensory
RT neuron-specific GPCRs.";
RL Nat. Neurosci. 5:201-209(2002).
DR EMBL; AF474989; AAL86880.2; -.
DR GO:0016021; C:integral to membrane; IEA.
DR GO:0004872; F:receptor activity; IEA.
DR GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
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DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm1.1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
DR Receptor.
KW Receptor.
SQ SEQUENCE 322 AA; 36423 MW; 3D6FFB4B5DDFD90 CRC64;

Query Match
Best Local Similarity 81.9%; Score 1382; DB 4; Length 322;
Matches 268; Conservative 20; Mismatches 32; Indels 0; Gaps 0;

QY 1 MDSTIPVLGTELPIINGREETPCYKQTLSTGLTICIVSLVALTGNAVVLWLLGCRMRNA 60
Db 1 MDPTVPVLGKLTPIINGREETPCYKQTLSTGLTICIVSLVALTGNAVVLWLLGCRMRNA 60
QY 61 VSIYILNLVAADFLFSGHIIICSPRLINIRHPISKILSPVMTFFPYFGLSMLSAISTER 120
Db 61 VSIYILNLVAADFLFSGHIIICSPRLINIRHPISKILSPVMTFFPYFGLSMLSAISTER 120
QY 121 CLSILMPIWYHCRPRYLSSVMCVLLWALSLLSILEWMFCDFLFGSADSVWCETSDFIT 180
Db 121 CLSILMPIWYHCRPRYLSSVMCVLLWALSLLSILEWMFCDFLFGSADSVWCETSDFIT 180
QY 181 IAWLVFLCVVLCGSSLLVRLICGSRKMPLETRLYVTILLTVLVFLLCGLPFGIQWALFS 240
Db 181 IAWLVFLCVVLCGSSLLVRLICGSRKMPLETRLYVTILLTVLVFLLCGLPFGIQWALFS 240
QY 241 RIHLDWKVLFCHVHLVIFLSALNSSANPIIYFVGSFRQRQRNLKLVLRALQDTP 300
Db 241 RIHLDWKVLFCHVHLVIFLSALNSSANPIIYFVGSFRQRQRNLKLVLRALQDTP 300
QY 301 VDEGGWLPQETLELSGRLEQ 322
Db 301 VDEGGWLPQETLELSGRLEQ 322

RESULT 8
Q96LA9 PRELIMINARY; PRT; 322 AA.
AC Q96LA9
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE G protein-coupled receptor.
GN MRGX4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21435808; PubMed=11551509;
DR Dong X., Han S.-K., Zylka M.J., Simon M.I., Anderson D.J.;
RT "A Diverse Family of GPCRs Expressed in Specific Subsets of
RT Nociceptive Somatosensory Neurons.";
RL Cell 106:619-632(2001).
DR EMBL; AY042216; AAK91807.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1.1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 322 AA; 36434 MW; 7CA676F8BD390A31 CRC64;

Query Match
Best Local Similarity 81.0%; Score 1367; DB 4; Length 322;
Matches 266; Conservative 20; Mismatches 34; Indels 0; Gaps 0;

QY 1 MDSTIPVLGTELPIINGREETPCYKQTLSTGLTICIVSLVALTGNAVVLWLLGCRMRNA 60
Db 1 MDPTVPVLGKLTPIINGREETPCYKQTLSTGLTICIVSLVALTGNAVVLWLLGCRMRNA 60
QY 61 VSIYILNLVAADFLFSGHIIICSPRLINIRHPISKILSPVMTFFPYFGLSMLSAISTER 120
Db 61 VSIYILNLVAADFLFSGHIIICSPRLINIRHPISKILSPVMTFFPYFGLSMLSAISTER 120
QY 121 CLSILMPIWYHCRPRYLSSVMCVLLWALSLLSILEWMFCDFLFGSADSVWCETSDFIT 180
Db 121 CLSILMPIWYHCRPRYLSSVMCVLLWALSLLSILEWMFCDFLFGSADSVWCETSDFIT 180
QY 181 IAWLVFLCVVLCGSSLLVRLICGSRKMPLETRLYVTILLTVLVFLLCGLPFGIQWALFS 240
Db 181 IAWLVFLCVVLCGSSLLVRLICGSRKMPLETRLYVTILLTVLVFLLCGLPFGIQWALFS 240
QY 241 RIHLDWKVLFCHVHLVIFLSALNSSANPIIYFVGSFRQRQRNLKLVLRALQDTP 300
Db 241 RIHLDWKVLFCHVHLVIFLSALNSSANPIIYFVGSFRQRQRNLKLVLRALQDTP 300
QY 301 VDEGGWLPQETLELSGRLEQ 322
Db 301 VDEGGWLPQETLELSGRLEQ 322

RESULT 7
Q8TDD8 PRELIMINARY; PRT; 322 AA.
AC Q8TDD8
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE G protein-coupled receptor SNR4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21853733; PubMed=11850634;
DR Lenbo B.M., Grazzini E., Groblewski T., O'Donnell D., Roy M.-O.,
DR Zhang J., Hofert C., Cao J., Schmidt R., Pelletier M., Labarre M.,
DR Gosselin M., Fortin Y., Banville D., Shen S., Strom P., Payza K.,
DR Dray A., Walker P., Ahmad S.;
RT "Proenkephalin A gene products activate a new family of sensory
RT neuron-specific GPCRs.";
RL Nat. Neurosci. 5:201-205(2002).
DR EMBL; AF474990; AAJ86881.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1.1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 322 AA; 36236 MW; C301BC174BB01D72 CRC64;

Query Match
Best Local Similarity 81.9%; Score 1382; DB 4; Length 322;
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Db 175 GSGWCQTFDFAAALIFLFWLVCSSALVRLCGSRGLPRLYLTLTLVLFLL 234
QY 228 CGLPFGIQWALFSRIHLDKWLFCFHVHVSIFLSALNSSANPIIYFFVGSFRQNRQN- 286
Db 235 CGLPFGIQWFLILWIKWSDVLFCHHPVSIVLSSINSSANPIIYFFVGSFRKQRLQOP 294
QY 287 -LKLVLQRLALQDTPEVDEGGWLPQETLELSGRL 320
Db 295 ILKLALQRLALQDIAEVDHSGCFRQGTPEMSRSL 329

RESULT 11
Q7TN42 PRELIMINARY; PRT; 323 AA.
AC Q7TN42;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE MRGC G protein-coupled receptor.
GN MRGC.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=22810130; PubMed=12909716;
RA Ziyka M.J., Dong X., Southwell A.L., Anderson D.J.;
RT "Atypical expansion in mice of the sensory neuron-specific Mrg G
protein-coupled receptor family."
RL Proc. Natl. Acad. Sci. U.S.A. 100:10043-10048 (2003).
DR EMBL; AF518245; AAQ08317.1; -.
KW Receptor.
SQ SEQUENCE 323 AA; 50639FDAE42E8052 CRC64;

Query Match 48.8%; Score 823.5; DB 11; Length 323;
Best Local Similarity 52.8%; Pred. No. 6.7e-65;
Matches 172; Conservative 51; Mismatches 92; Indels 11; Gaps 6;

QY 1 MDSTIPVLGTLPINGREETPCYKOTLSFTGTCIVSLVALTGNVAVLWLLGCRMRNA 60
Db 1 MDPTISLSTESTLNKTGHPSC-RPILTLFSLVPIITLLGLAGNTIVLWLLGFRMRKA 59
QY 61 VSIYILNLVAADFSLGHIICSPRLINI----RHPISK-ILSPWMTFFYFGLSMLSA 115
Db 60 ISVYVNLNLSDSFFLCCHPIDSIMRMNFIYAHKLSKEILGNVAFIPYISGLSIISA 119
QY 116 ISTERCLSIILWPIWYHCHRRPRYSVVMCVLLWALSILRSILEWMCDFLPSGADSVWCET 175
Db 120 ISTERCLSVLWPIWYHCHRRPRNMSAICVLIVLWLSFLMGILDWFFSGFLGETHHLM-KN 178
QY 176 SDFITIAWLVLCVLCGSSLVLLVRLCGSRKMPRLTRLYVTILLTVLFLCGLPFGIQ 235
Db 179 VDFIVTAFILFLFMLFGSSALLVRLCGSRKPLSRLYVTISLVVWVLLCGLPLGY 238
QY 236 WAL--FSRIHLDKWLFCFHVHVSIFLSALNSSANPIIYFFVGSFRQNRQNLKVLOR 293
Db 239 LFLLYWFGIHLHP--FCHIVQTVLLSCVNSSANPIIYFVGSFRHKKHRSKMLVKR 296
QY 294 ALQDTPVDEGGWLPQETLELSGSR 319
Db 297 ALBETPEDEYTDHVKQKTEISERR 322

RESULT 12
Q8R4G1 PRELIMINARY; PRT; 337 AA.
AC Q8R4G1;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE MRGC G protein-coupled receptor.
GN MRGC.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=22810130; PubMed=12909716;
RA Ziyka M.J., Dong X., Southwell A.L., Anderson D.J.;
RT "Atypical expansion in mice of the sensory neuron-specific Mrg G
protein-coupled receptor family."
RL Proc. Natl. Acad. Sci. U.S.A. 100:10043-10048 (2003).
DR EMBL; AF518245; AAQ08317.1; -.
KW Receptor.
SQ SEQUENCE 337 AA; 50639FDAE42E8052 CRC64;

Query Match 48.6%; Score 820.5; DB 11; Length 337;
Best Local Similarity 52.5%; Pred. No. 1.3e-64;
Matches 171; Conservative 51; Mismatches 93; Indels 11; Gaps 6;

QY 1 MDSTIPVLGTLPINGREETPCYKOTLSFTGTCIVSLVALTGNVAVLWLLGCRMRNA 60
Db 15 MDPTISLSTESTLNKTGHPSC-RPILTLFSLVPIITLLGLAGNTIVLWLLGFRMRKA 73
QY 61 VSIYILNLVAADFSLGHIICSPRLINI----RHPISK-ILSPWMTFFYFGLSMLSA 115
Db 74 ISVYVNLNLSDSFFLCCHPIDSIMRMNFIYAHKLSKEILGNAAIIPYISGLSIISA 133
QY 116 ISTERCLSIILWPIWYHCHRRPRYSVVMCVLLWALSILRSILEWMCDFLPSGADSVWCET 175
Db 134 ISTERCLSVLWPIWYHCHRRPRNMSAICVLIVLWLSFLMGILDWFFSGFLGETHHLM-KN 192
QY 176 SDFITIAWLVLCVLCGSSLVLLVRLCGSRKMPRLTRLYVTILLTVLFLCGLPFGIQ 235
Db 193 VDFIVTAFILFLFMLFGSSALLVRLCGSRKPLSRLYVTISLVVWVLLCGLPLGY 252
QY 236 WAL--FSRIHLDKWLFCFHVHVSIFLSALNSSANPIIYFFVGSFRQNRQNLKVLOR 293
Db 253 LFLLYWFGIHLHP--FCHIVQTVLLSCVNSSANPIIYFVGSFRHKKHRSKMLVKR 310
QY 294 ALQDTPVDEGGWLPQETLELSGSR 319
Db 311 ALBETPEDEYTDHVKQKTEISERR 336

RESULT 13
Q8CIP3 PRELIMINARY; PRT; 322 AA.
AC Q8CIP3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE G protein-coupled receptor MrgC11.
GN MRGC11.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=22317401; PubMed=12397184;
RA Han S.K., Dong X., Hwang J.I., Ziyka M.J., Anderson D.J., Simon M.I.;
RT "Orphan G protein-coupled receptors MrgA1 and MrgC11 are distinctively
activated by RF-amide-related peptides through the Galpha q/11
pathway."
RL Proc. Natl. Acad. Sci. U.S.A. 99:14740-14745 (2002).
DR EMBL; AY152435; AAN64385.1; -.
KW GO:0016021; C:integral to membrane; IEA.
GO: GO:0016021; C:integral to membrane; IEA.
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DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO: GO:0007185; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G-PROTEIN RECP_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN RECP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 322 AA; 36809 MW; 1E03ECD544AF86DC CRC64;

Query Match
Best Local Similarity 47.2%; Score 797; DB 11; Length 322;
Matches 174; Conservative 43; Mismatches 96; Indels 14; Gaps 8;

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DB 1 MDPTSSHDTESTPLNETGHPNCTPILTLSP--LVLTITVLGLAGNTIVLWLLGFRMRK 58

QY 60 AVSIYILNLVAADFLSLGSHIICSPRLINI-----RHPISK-IISPVMTFFYFGLSMLS 114
DB 59 AISVILNLALADSFLLCHFDISLRLIIDFYGLVAHKLSDILGNAAIIFYISGLSILS 118

QY 115 AISTERCILWPIWYHCHRRPYLSSVMCVLLWALSILRSILEWFCDFLPSGADSVWCE 174
DB 119 AISTERCILWPIWYHCHRRPYLSSVMCVLLWALSILRSILEWFCDFLPSGADSVWCE 176

QY 175 TDSFTITIAWLVFLCVLWCGSSLVLLVRLICGSRKMPLTRLYVTILLTVLVLGCLPGL 234
DB 177 NVDFITITIAWLVFLCVLWCGSSLVLLVRLICGSRKMPLTRLYVTILLTVLVLGCLPGL 236

QY 235 QWAL--FSRIHLDWKVLFCHVHLSIFLSALNSSANPIIYFVSGFRQRONKILVLQ 292
DB 237 YLFLLYFQVHLHYF--FCHIQVAVLSCVNSSANPIIYFVSGFRQRONKILVLQ 294

QY 293 RALQDTPEVDEGGWLPQETLLELSGR 319
DB 295 RALQDTPEVDEGGWLPQETLLELSGR 321

RESULT 14
Q7TN49 PRELIMINARY; PRT; 304 AA.
AC Q7TN49;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE MRGA G protein-coupled receptor.
GN MRGA.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RT "Cloning and functional characterization of the rat orphan GPCR
RT rc 56.1.3."
RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ311952; CAC84592.1; -.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO: GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G-PROTEIN RECP_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN RECP_F1_2; 1.
KW G-protein coupled receptor; Receptor.
SQ SEQUENCE 331 AA; 37005 MW; 74BAE8C557859AC CRC64;

Query Match
Best Local Similarity 46.1%; Score 778; DB 11; Length 331;
Matches 176; Conservative 33; Mismatches 85; Indels 36; Gaps 8;

QY 1 MDSTIPVLGTELPINGREETPCYKQTLSTGLTCTIVS-LVALTGNVVLWLLGCMRRN 59
DB 28 MDXTIP-----GSFNGRTLP-----NLLIISGLVGLIGNAMVFWLLGFLARN 72

QY 60 AVSIYILNLVAADFLSLGSHIICSPRLINIHP-----ISKILSPVMTFFYFGLSMLS 116
DB 73 AFSVILNLALADFLFLCHIIDSTLLLLKFSYPNIIFPCFTVMVWYIAGLSMLS 132

QY 117 STERCILSWPIWYHCHRRPYLSSVMCVLLWALSILRSILEWFCDFLPSGADSVW---- 172
DB 133 STERCILSWPIWYHCHRRPYLSSVMCVLLWALSILRSILEWFCDFLPSGADSVW---- 172

QY 173 -CETSDFTITIAWLVFLCVLWCGSSLVLLVRLICGSRKMPLTRLYVTILLTVLVLGCLP 231
DB 189 RCLASNEFTTACLTFLFVVLVCLSLALLVRSFQAGRMKLTRLYATIMLTIVLVLGCLP 248

Query Match
Best Local Similarity 53.3%; Pred. No. 7.3e-61;
Matches 176; Conservative 33; Mismatches 85; Indels 36; Gaps 8;

QY 1 MDSTIPVLGTELPINGREETPCYKQTLSTGLTCTIVS-LVALTGNVVLWLLGCMRRN 59
DB 28 MDXTIP-----GSFNGRTLP-----NLLIISGLVGLIGNAMVFWLLGFLARN 72

QY 60 AVSIYILNLVAADFLSLGSHIICSPRLINIHP-----ISKILSPVMTFFYFGLSMLS 116
DB 73 AFSVILNLALADFLFLCHIIDSTLLLLKFSYPNIIFPCFTVMVWYIAGLSMLS 132

QY 117 STERCILSWPIWYHCHRRPYLSSVMCVLLWALSILRSILEWFCDFLPSGADSVW---- 172
DB 133 STERCILSWPIWYHCHRRPYLSSVMCVLLWALSILRSILEWFCDFLPSGADSVW---- 172

QY 173 -CETSDFTITIAWLVFLCVLWCGSSLVLLVRLICGSRKMPLTRLYVTILLTVLVLGCLP 231
DB 189 RCLASNEFTTACLTFLFVVLVCLSLALLVRSFQAGRMKLTRLYATIMLTIVLVLGCLP 248

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Job time : 73 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 4, 2004, 04:48:57 ; Search time 4166 Seconds
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Perfect score: 969
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 2167151695 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: gb.htg.*
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- 8: gb.pl.*
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- 11: gb.sts.*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	969	100.0	969	6	AX498196	AX498196 Sequence
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4	969	100.0	1400	6	AX549388	AX549388 Sequence
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6	969	100.0	2618	6	AX429465	AX429465 Sequence
7	969	100.0	8622	6	AX429467	AX429467 Sequence
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17	837.8	86.5	969	6	E40003	E40003 Novel G pro
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C 44	829.8	85.6	163718	9	AC023078	AC023078 Homo sapi
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ALIGNMENTS

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LOCUS E43450 969 bp DNA linear PAT 31-JAN-2002
DEFINITION Novel protein G-coupled receptor protein and DNA thereof.
ACCESSION E43450
VERSION E43450.1 GI:18627716
KEYWORDS JP 2000166576-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 969)
AUTHORS Watanabe,T., Terao,S. and Matsui,H.
TITLE Novel protein G-coupled receptor protein and DNA thereof
JOURNAL Patent: Jp 2000166576-A 1 20-JUN-2000;

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COMMENT
TAKEDA CHEM IND LTD
OS Homo sapiens (human)
PN JP 2000166576-A/1
PD 20-JUN-2000
PF 30-SEP-1999 JP 1999278116
PR TAKUYA WATANABE,SHIZUKO TERA0,HIDEKI MATSUI
PC C12N15/09,A61K38/00,A61K39/395,A61K45/00,A61K48/00,
PC A61P43/00,
PC C07K14/705,C07K16/28,C12N1/21,C12N5/10,C12P21/02,C12P21/08,PC
G01N33/15,
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C12R1:91),
PC (C12P21/02,C12R1:19),(C12P21/08,C12R1:91),C12N15/00,A61K37/02,
PC C12N5/00,
PC (C12N5/00,C12R1:91)
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RESULT 2
AX498196 969 bp DNA linear PAT 26-SEP-2002
LOCUS
DEFINITION
Sequence 19 from Patent WO242461.
ACCESSION AX498196
VERSION AX498196.1 GI:23343119
KEYWORDS
SYNTHETIC CONSTRUCT
ORGANISM
synthetic construct
artificial sequences.
REFERENCE
1 Chen,R., Chu,Z.L., Dang,H.T., Lowitz,K.P. and Pride,C.
AUTHORS Endogenous and non-endogenous versions of human g protein-coupled
TITLE receptors
JOURNAL Patent: WO 0242461-A 19 30-MAY-2002;
Arena Pharmaceuticals, Inc. (US)
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Query Match 100.0%; Score 969; DB 6; Length 969;
Best Local Similarity 100.0%; Pred. No. 1e-244;
Matches 969; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATTCAACCATCCAGCTTGGGTACAGAACTGACACCAATCAACGACGTGAGGAG 60
DB 1 ATGATTCAACCATCCAGCTTGGGTACAGAACTGACACCAATCAACGACGTGAGGAG 60
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Db 1232 GTGGATGAAGGTGGAGGTGGCTTCTCTCAGGAACCCCTGGAGCTCTCGGAGACAGATTG 1291
QY 961 GAGCAGTGA 969
Db 1292 GAGCAGTGA 1300

RESULT 4
AX549388
LOCUS AX549388 1400 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 673 from Patent WO02061087.
ACCESSION AX549388
VERSION AX549388.1 GI:25814004
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
AUTHORS
REFERENCE 1
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE
Antigenic peptides, such as for G protein-coupled receptors
(GPCRs), antibodies thereto, and systems for identifying such
antigenic peptides
JOURNAL Patient: WO 02061087-A 673 08-AUG-2002;
Lifespan Biosciences, Inc. (US)
FEATURES
source
1. .1400
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 100.0%; Score 969; DB 6; Length 1400;
Best Local Similarity 100.0%; Pred. No. 1.1e-244;
Matches 969; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGATTCAACATCCAGTCTTGGGTACAGAACTGACACCAATCAACGAGCTGAGGAG 60
Db 332 ATGGATTCAACATCCAGTCTTGGGTACAGAACTGACACCAATCAACGAGCTGAGGAG 391
QY 61 ACTCCTTGCTACAGACAGACCTGAGCTTCAAGGGCTGACGTGATCGTTTCCCTTGTC 120
Db 392 ACTCCTTGCTACAGACAGACCTGAGCTTCAAGGGCTGACGTGATCGTTTCCCTTGTC 451
QY 121 GCCTGACAGAAACGCGTGTGCTCTGCTCTGCTGGCTGGCGATGCGGACGACGCT 180
Db 452 GCCTGACAGAAACGCGTGTGCTCTGCTCTGCTGGCTGGCGATGCGGACGACGCT 511
QY 181 GTCTCCATCTACATCTCAACCTGTCGGGGCGAGCTTCTCTCTTCTAGCGGCCACATT 240
Db 512 GTCTCCATCTACATCTCAACCTGTCGGGGCGAGCTTCTCTCTTCTAGCGGCCACATT 571
QY 241 ATATGTTGCGGTTAGCGCTCATCAATATCCGCCATCCCATCTCCAAAATCTCAGTCT 300
Db 572 ATATGTTGCGGTTAGCGCTCATCAATATCCGCCATCCCATCTCCAAAATCTCAGTCT 631
QY 301 GTGATGACCTTCCCTACTTTATAGGCTTAAGCATCTGAGCGCCATCAGACCGAGCGC 360
Db 632 GTGATGACCTTCCCTACTTTATAGGCTTAAGCATCTGAGCGCCATCAGACCGAGCGC 691
QY 361 TGCTGTGCCATCTGTGGCCCATCTGTAACACTTGGCGCGCCGCCAGACCTGTGCATCG 420
Db 692 TGCTGTGCCATCTGTGGCCCATCTGTAACACTTGGCGCGCCGCCAGACCTGTGCATCG 751
QY 421 GTCATGTGTCTGCTCTGGGCGCTGCTCCTGCTGGGAGTATCTCGAGTGGATGTTTC 480
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QY 481 TGTGACTTCTCTGTTTAGTGTGCTGATTCTGTTTGTGTGAAACGTCAGATTTCATTACA 540
Db 812 TGTGACTTCTCTGTTTAGTGTGCTGATTCTGTTTGTGTGAAACGTCAGATTTCATTACA 871
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QY 661 ACAGTGTGCTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
Db 992 ACAGTGTGCTCTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1051
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Db 1112 TCCGCTCTTAACAGAGTGCACCAACCCCATCAATTACTTCTGCTGGGCTCTTTAGGCAG 1171
QY 841 CGTCAAAATAGGACAACTGAAAGCTGGTTCCTCAGAGGGCTCTGAGGACACGCTGAG 900
Db 1172 CGTCAAAATAGGACAACTGAAAGCTGGTTCCTCAGAGGGCTCTGAGGACACGCTGAG 1231
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Db 1292 GAGCAGTGA 1300

RESULT 5
AY042215
LOCUS AY042215 1400 bp DNA linear PRI 14-SEP-2001
DEFINITION Homo sapiens G protein-coupled receptor (MRGX3) gene, complete cds.
ACCESSION AY042215
VERSION AY042215.1 GI:15546055
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
AUTHORS
REFERENCE 1 (bases 1 to 1400)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE
A diverse family of GPCRs expressed in specific subsets of
nociceptive sensory neurons
JOURNAL Cell 106 (5), 619-632 (2001)
MEDLINE 21435808
PubMed 11551509
REFERENCE 2 (bases 1 to 1400)
Dong, X., Han, S.-K., Zylka, M.J., Simon, M.I. and Anderson, D.J.
Direct Submission
Submitted (19-JUN-2001) Division of Biology, 216-76, California
Institute of Technology, 1201 E. California Blvd., Pasadena, CA
91125, USA
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source
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ORIGIN		
Query Match	100.0%; Score 969; DB 9; Length 1400;	
Best Local Similarity	100.0%; Pred. No. 1.1e-244;	
Matches 969; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 ATGGATTCAACCATCCAGTCTTGGGTACAGAACTGACACCAATCAACGGACGTGAGGAG 60	
Db	332 ATGGATTCAACCATCCAGTCTTGGGTACAGAACTGACACCAATCAACGGACGTGAGGAG 391	
Qy	61 ACTCCTTGCTACAGAGACCTGAGCTTACGGGGCTGAGGTGATCGTTCCTTGTGTC 120	
Db	392 ACTCCTTGCTACAGAGACCTGAGCTTACGGGGCTGAGGTGATCGTTCCTTGTGTC 451	
Qy	121 GCGCTGACAGGAAACCGGCTTGTCTGGCTCTCGGCTGCGCATCGCAGGAACGCT 180	
Db	452 GCGCTGACAGGAAACCGGCTTGTCTGGCTCTCGGCTGCGCATCGCAGGAACGCT 511	
Qy	181 GTCTCATCTACATCCTCAACCTGTGCGGGCGGACCTTCTCTTCTAGCGGCAATT 240	
Db	512 GTCTCATCTACATCCTCAACCTGTGCGGGCGGACCTTCTCTTCTAGCGGCAATT 571	
Qy	241 ATATGTTGCGGTTACGCTCATCAATATCGCCATCCCATCTCCAAATCCTCAGTCT 300	
Db	572 ATATGTTGCGGTTACGCTCATCAATATCGCCATCCCATCTCCAAATCCTCAGTCT 631	
Qy	301 GTGATGACCTTCCCTACTTTATAGCCCTAAGCATGCTAGCGGCATCAGCACCGAGCGC 360	
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Qy	361 TGCGTGTCCATCCTGTGCGCCATCTGTACCACTGCGCGCCCGCCAGATCCTGTCATCG 420	
Db	692 TGCGTGTCCATCCTGTGCGCCATCTGTACCACTGCGCGCCCGCCAGATCCTGTCATCG 751	
Qy	421 GTCATGTGTGTCCTGCTGCGCCCTGTCCTGCTGCGAGTATCCTGGAGTGGATGTC 480	
Db	752 GTCATGTGTGTCCTGCTGCGCCCTGTCCTGCTGCGAGTATCCTGGAGTGGATGTC 811	
Qy	481 TGTGACTTCTCTTAGTGGTCTGATTTCTGTTGGTGGAACGTGAGATTCATTACA 540	
Db	812 TGTGACTTCTCTTAGTGGTCTGATTTCTGTTGGTGGAACGTGAGATTCATTACA 871	
Qy	541 ATCGGCTGGCTGGTGTGTTTATGTTGTTCTCTGTTGGGTCCAGCTGCTGCTGTC 600	
Db	872 ATCGGCTGGCTGGTGTGTTTATGTTGTTCTCTGTTGGGTCCAGCTGCTGCTGTC 931	
Qy	601 AGGATCTCTGTGGATCCCGGAAGATGCGGCTGACAGCGTGATCGTGACCATCTCTC 660	
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Qy	661 ACAGTGTGCTGCTTCTCTCTCTGTGGCTGCGCTTGGCATTCAGTGGCGCTGTTTCC 720	
Db	992 ACAGTGTGCTGCTTCTCTCTCTGTGGCTGCGCTTGGCATTCAGTGGCGCTGTTTCC 1051	
Qy	721 AGGATCCACTGGATGGAAAGTCTTATTTGTGATGTGATCTAGTTTCCATTTCTG 780	
Db	1052 AGGATCCACTGGATGGAAAGTCTTATTTGTGATGTGATCTAGTTTCCATTTCTG 1111	
Qy	781 TCGGCTCTTAAAGAGAGTGGCAACCCATCATTTACTTCTGCTGGCTCTTTAGGAG 840	

Db	1112 TCCGCTCTTAAACAGCAGTGCACCCCATCATTTACTTCTTCTGGGTCTCTTTAGGCAG 1171	
Qy	841 CGTCAAAATAGGCAGAACCTGAGCTGGTTTCCAGAGGGCTCTGAGACACGCTGAG 900	
Db	1172 CGTCAAAATAGGCAGAACCTGAGCTGGTTTCCAGAGGGCTCTGAGACACGCTGAG 1231	
Qy	901 GTGGATGAAGGTGACGGTGGCTTCTCAGGAAACCTCGAGAGTGTGCGGAAACAGATTG 960	
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Qy	961 GAGCAGTGA 969	
Db	1292 GAGCAGTGA 1300	
RESULT 6		
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LOCUS	Sequence 1 from Patent WO0234914.	linear
DEFINITION	AX429465	PAT 21-JUN-2002
ACCESSION	AX429465	
VERSION	AX429465.1	GI:21540763
KEYWORDS	Homo sapiens (human)	
SOURCE	Homo sapiens	
ORGANISM	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	1	
AUTHORS	Zhao,Q., Beasley,E.M. and Wei,M.H.	
TITLE	Isolated human g-protein coupled receptors, nucleic acid molecules encoding human gpr proteins, and uses thereof	
JOURNAL	Patent: WO 0234914-A 1 02-MAY-2002;	
PE CORP NY (US)		
FEATURES	Location/Qualifiers	
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Best Local Similarity	100.0%; Pred. No. 1.2e-244;	
Matches 969; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 ATGGATTCAACCATCCAGTCTTGGGTACAGAACTGACACCAATCAACGGACGTGAGGAG 60	
Db	492 ATGGATTCAACCATCCAGTCTTGGGTACAGAACTGACACCAATCAACGGACGTGAGGAG 551	
Qy	61 ACTCCTTGCTACAGAGACCTGAGCTTCACGGGCTGACGTGCAATCGTTTCCCTTGTGTC 120	
Db	552 ACTCCTTGCTACAGAGACCTGAGCTTCACGGGCTGACGTGCAATCGTTTCCCTTGTGTC 611	
Qy	121 GCGCTGACAGGAAACCGGTTGTCTGCTCCTGGGCTGCGCATGCGCAGGAACGCT 180	
Db	612 GCGCTGACAGGAAACCGGTTGTCTGCTCCTGGGCTGCGCATGCGCAGGAACGCT 671	
Qy	181 GTCTCCATCTACATCCTCAACCTGGTTCGGGCGGACCTTCTCTTCTTACGCGCCACATT 240	
Db	672 GTCTCCATCTACATCCTCAACCTGGTTCGGGCGGACCTTCTCTTCTTACGCGCCACATT 731	
Qy	241 ATATGTTGCGGTTAGCGCTCATCATATCCGCCATCCCATCTCGAAATCTCAGTCTCT 300	
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Qy	301 GTATGACCTTTCCTTACTTTATAGCCCTAAGCATGCTGAGCGCCATCAGCACCGAGCGC 360	
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Qy	361 TGCGTGTCCATCTCTGTGGCCCATCTGGTACCATCTGCGCGCCGCCAGATACCTGTATCG 420	
Db	852 TGCGTGTCCATCTCTGTGGCCCATCTGGTACCATCTGCGCGCCGCCAGATACCTGTATCG 911	
Qy	421 GTCATGTGTCTGCTCTGCGGCCCTGTCCTCTGCTGCGAGTATCCTTGGAGTGGATGTC 480	

Db	912	GTCTGTGTCTGCTGCTGGGCCCTGTCCTGCTGGAGTATCCTGGAGTGAATTC	971
Qy	481	TGTGATCTCTGTTAGTGGTCTGATTTCTGTTTGGTGTGAACCTCAGATTTCATTACA	540
Db	972	TGTGATCTCTGTTAGTGGTCTGATTTCTGTTTGGTGTGAACCTCAGATTTCATTACA	1031
Qy	541	ATCGCGTGTGCTGTTTATTTATGTTGTTCTCTGTTGGTCCAGCTGTGCTGTGCTG	600
Db	1032	ATCGCGTGTGCTGTTTATTTATGTTGTTCTCTGTTGGTCCAGCTGTGCTGTGCTG	1091
Qy	601	AGGATCTCTGTGGATCCCGGAAGATGCCGCTGACAGGCTGTAGTGAACATCTCTCTC	660
Db	1092	AGGATCTCTGTGGATCCCGGAAGATGCCGCTGACAGGCTGTAGTGAACATCTCTCTC	1151
Qy	661	ACAGTCTGTGCT	720
Db	1152	ACAGTCTGTGCT	1211
Qy	721	AGGATCCACTGGATTGGAAGTCTTATTTGTGATGTCATCTAGTTTCCATTTTCTCTG	780
Db	1212	AGGATCCACTGGATTGGAAGTCTTATTTGTGATGTCATCTAGTTTCCATTTTCTCTG	1271
Qy	781	TCCGCTCTTAACAGCAGTGCACACCCCATCTTCTCTCTCTCTCTCTCTCTCTCTCTCT	840
Db	1272	TCCGCTCTTAACAGCAGTGCACACCCCATCTTCTCTCTCTCTCTCTCTCTCTCTCTCT	1331
Qy	841	CGTCAAAATAGGAGAACCTGAAGCTGTTCTCCAGAGGCTCTGACAGACAGCCTGAG	900
Db	1332	CGTCAAAATAGGAGAACCTGAAGCTGTTCTCCAGAGGCTCTGACAGACAGCCTGAG	1391
Qy	901	GTGGATGAAGTGGAGGGTGGCTTCTCTCAGGAACCTGGAGCTGCGGAGACGAGATTG	960
Db	1392	GTGGATGAAGTGGAGGGTGGCTTCTCTCAGGAACCTGGAGCTGCGGAGACGAGATTG	1451
Qy	961	GAGCAGTGA 969	
Db	1452	GAGCAGTGA 1460	
RESULT 7			
AX429467			
LOCUS	AX429467	8622 bp	DNA linear PAT 21-JUN-2002
DEFINITION	Sequence 3 from Patent WO0234914.		
ACCESSION	AX429467		
VERSION	AX429467.1	GI:21540764	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE			
AUTHORS	Zhao, Q., Beasley, E.M. and Wei, M.H.		
TITLE	Isolated human g-protein coupled receptors, nucleic acid molecules encoding human gpcr proteins, and uses thereof		
JOURNAL	Patent: WO 0234914-A 3 02-MAY-2002;		
PE CORP NY (US)			
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Qy	1	ATGGATTCAACATCCAGTCTTGGTACAGAACTGACCAATCAACGACGCTGAGAG	60
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Db	7588	ACTCTTGTCTACAAGCAGACCCCTGAGCTTCAAGGGCTGACGTGATCTTCCCTTGTG	7647
Qy	121	GCCTGACAGAAACGGGTTGCTCTGCTCTGGGTGCGCATGCGCAGAAACGCT	180
Db	7648	GCCTGACAGAAACGGGTTGCTCTGCTCTGGGTGCGCATGCGCAGAAACGCT	7707
Qy	181	GTCTCCATCTACATCTCAACCTGGTGGGGCGGACTTCTCTTCTTCTAGCGCCACT	240
Db	7708	GTCTCCATCTACATCTCAACCTGGTGGGGCGGACTTCTCTTCTTCTAGCGCCACT	7767
Qy	241	ATATGTTGCGCGTTAGCCTCATATATCGGCATCCCATCTCCAAAATCCCTCAGTCCT	300
Db	7768	ATATGTTGCGCGTTAGCCTCATATATCGGCATCCCATCTCCAAAATCCCTCAGTCCT	7827
Qy	301	GTGATGACCTTTCCCTACTTTATAGGCTTAAGCATGCTAGAGCCATFAGCAACGAGCGC	360
Db	7828	GTGATGACCTTTCCCTACTTTATAGGCTTAAGCATGCTAGAGCCATFAGCAACGAGCGC	7887
Qy	361	TGCTGTGCT	420
Db	7888	TGCTGTGCT	7947
Qy	421	GTGATGCTGTCT	480
Db	7948	GTGATGCTGTCT	8007
Qy	481	TGTGATCT	540
Db	8008	TGTGATCT	8067
Qy	541	ATCGCGTGGCTGTTTTTTTTTATGTTGTTCTCTCTGGGTCCAGCTGGCTCTCTCTCTCT	600
Db	8068	ATCGCGTGGCTGTTTTTTTTTATGTTGTTCTCTCTGGGTCCAGCTGGCTCTCTCTCTCT	8127
Qy	601	AGGATCTCTCTGATCCCGAAGATCCCGTACCGCTGACGAGCTGACGTGACCATCTCTCTC	660
Db	8128	AGGATCTCTCTGATCCCGAAGATCCCGTACCGCTGACGAGCTGACGTGACCATCTCTCTC	8187
Qy	661	ACAGTCTGTGCTTCT	720
Db	8188	ACAGTCTGTGCTTCT	8247
Qy	721	AGGATCCACCTGGATGGAAGTCTTATTTGTGATGTCATGTCATGTCATGTCATGTCATG	780
Db	8248	AGGATCCACCTGGATGGAAGTCTTATTTGTGATGTCATGTCATGTCATGTCATGTCATG	8307
Qy	781	TCCGCTCTTAACAGCAGTGCACACCCCATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	840
Db	8308	TCCGCTCTTAACAGCAGTGCACACCCCATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	8367
Qy	841	CCTCAAAATAGCAGAACCTGAGCTGTTCTCCAGAGGGCTCTCCAGGACACGCTCTGAG	900
Db	8368	CCTCAAAATAGCAGAACCTGAGCTGTTCTCCAGAGGGCTCTCCAGGACACGCTCTGAG	8427
Qy	901	GTGGATGAAGTGGAGGGTGGCTTCTCAGGAACCTCGGAGCTGTCCGGAGCAGATTG	960
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Qy	961	GAGCAGTGA 969	
Db	8488	GAGCAGTGA 8496	
RESULT 8			
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LOCUS	E43451	969 bp	DNA linear PAT 31-JAN-2002
DEFINITION	Novel protein G-coupled receptor protein and DNA thereof.		
ACCESSION	E43451		
VERSION	E43451.1	GI:18627717	
KEYWORDS	JP 200016576-A/2.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 969)
Watanabe,T., Texao,S. and Matsui,H.
Novel protein G-coupled receptor protein and DNA thereof
Patent: JP 2000166576-A 2 20-JUN-2000;
TAKEDA CHEM IND LTD
OS Homo sapiens (human)
PN JP 2000166576-A/2
PD 20-JUN-2000
PF 30-SEP-1999 JP 1999278116
PR
PI TAKUYA WATANABE, SHIZUKO TERAOKA, HIDEKI MATSUI
PC C12N15/09,A61K38/00,A61K39/395,A61K39/395,A61K45/00,A61K48/00,
PC A61P43/00,
PC C07K14/705,C07K16/28,C12N1/21,C12N5/10,C12P21/02,C12P21/08, PC
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C12R1:19),
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Query Match 99.8%; Score 967.4; DB 6; Length 969;
Best Local Similarity 99.9%; Pred. No. 2.7e-244;
Matches 968; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGATTCAACCATCCAGTCTTGGTACAGAACTGACACCAATCAACGGACGTGAGGAG 60
DB 1 ATGGATTCAACCATCCAGTCTTGGTACAGAACTGACACCAATCAACGGACGTGAGGAG 60

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QY 121 GCGCTGACAGGAAACGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
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DB 181 GTCTCATCTACATCTCAACCTGTCGCGGCGGACTTCTCTTCTTCTTCTTCTTCTTCTTCTTCT 240

QY 241 ATATGTTGCGGTTAGCGCTCATCAATATCGCCATCCCATCTCCAAATCCTCAGTCTCT 300
DB 241 ATATGTTGCGGTTAGCGCTCATCAATATCGCCATCCCATCTCCAAATCCTCAGTCTCT 300

QY 301 GTGATGACCTTTCCCTACTTTATAGGCTTATAGGCTTATAGGCTTATAGGCTTATAGGCTTAT 360
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QY 361 TCGCTGTCATCTGTCGCGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
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781 TCGCTCTTTAAACAGCAGTGTCCCAACCCCAATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 840
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841 CGTCAAAATAGGACAGACCTGAGCTGTTTCCAGAGGCTCTGAGGAGGCTCTGAGGAGGCTCTGAGGAGGCTCTGAG 900
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901 GTGGATGAAGTGGAGGCTGCTTCTCTCAGGAAACCCCTGAGCTGTCTGCGGAAACAGATTTG 960
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961 GAGCAGTGA 969
961 GAGCAGTGA 969

RESULT 9
AC108007/c
LOCUS
DEFINITION
AC108007
AC108007
VERSION
AC108007.5 GI:22655822
KEYWORDS
HTG.
SOURCE
Homo sapiens (human)
Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 91923)
Homo sapiens chromosome 11, clone CTD-3038L12, complete sequence.
AUTHORS
Birren,B., Nusbaum,C. and Lander,E.
TITLE
Homo sapiens chromosome 11, clone CTD-3038L12
JOURNAL
Unpublished
AUTHORS
2 (bases 1 to 91923)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Boguski,M., Bouckhuyt,B.,
Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
Choepel,Y., Collangelo,M., Collins,S., Collymore,A., Cook,A.,
Cooke,P., DeArrellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
Farrisa,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
Gande,S., Gird,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Horton,L., Huime,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., Lakocque,K., Lamazares,R.,
Lander,E., Leachman,A., Leachman,A., Levine,R., Liu,G., MacLean,C.,
Macdonald,P., Major,J., Marquis,N., Matthews,C., McCarthy,M.,
McEwan,P., McKernan,K., Meldrum,J., Meneus,L., Mihova,T.,
Mienka,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C.,
Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J.,
Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Roman,J.,
Retta,R., Rieback,M., Riley,K., Rise,C., Rogov,P., Roman,J.,
Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupbach,R., Seaman,S.,
Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Testaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Triglio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zemek,L., Zimmer,A. and Zody,M.
TITLE
Direct Submission
JOURNAL
Submitted (24-JAN-2002) Whitehead Institute/MIT Center for Genome

REFERENCE	Research, 320 Charles Street, Cambridge, MA 02141, USA	repeat_region	complement(251..899)
AUTHORS	3 (bases 1 to 91923)	repeat_region	/rpt family="L2"
	Birren,B., Nustbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,	repeat_region	900..1001
	Barina,N., Bastien,V., Bloom,T., Boguslavskiy,L., Boukhgalter,B.,	repeat_region	/rpt family="L1MD2"
	Camara,A., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,	repeat_region	1082..1655
	Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,	repeat_region	/rpt family="L1MD2"
	Faro,S., Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J.,	repeat_region	1671..1850
	Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B.,	repeat_region	/rpt family="L1MD3"
	Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A.,	repeat_region	complement(1858..1917)
	Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K.,	repeat_region	/rpt family="L2"
	Liu,G., Maclean,C., Macdonald,P., Major,J., Matthews,C.,	repeat_region	1918..2273
	McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,	repeat_region	/rpt family="THE1B"
	Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,	repeat_region	complement(2274..2327)
	O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K.,	repeat_region	/rpt family="L2"
	Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P.,	repeat_region	4505..4113
	Roman,J., Roy,A., Schauer,S., Schupback,R., Seaman,S., Severy,P.,	repeat_region	/rpt family="L2"
	Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J.,	repeat_region	5536..5795
	Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,	repeat_region	/rpt family="AluSc"
	Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,	repeat_region	5796..5837
	Zembek,L., Zimmer,A. and Zody,M.	repeat_region	/rpt family="(TAAA)n"
		repeat_region	5838..5875
TITLE	Direct Submission	repeat_region	/rpt family="AluSc"
JOURNAL	Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome	repeat_region	complement(7166..7526)
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REFERENCE	4 (bases 1 to 91923)	repeat_region	complement(10716..10825)
AUTHORS	Birren,B., Nustbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,	repeat_region	/rpt family="MIR"
	Barina,N., Bastien,V., Bloom,T., Boguslavskiy,L., Boukhgalter,B.,	repeat_region	11369..11466
	Camara,A., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,	repeat_region	/rpt family="L2"
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	Faro,S., Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J.,	repeat_region	/rpt family="MIR3"
	Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B.,	repeat_region	12072..12409
	Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A.,	repeat_region	/rpt family="MER2"
	Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K.,	repeat_region	12692..12875
	Liu,G., Maclean,C., Macdonald,P., Major,J., Matthews,C.,	repeat_region	/rpt family="LTR33"
	McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,	repeat_region	complement(12876..13294)
	Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,	repeat_region	/rpt family="MSTA"
	O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K.,	repeat_region	13255..13552
	Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P.,	repeat_region	/rpt family="LTR33"
	Roman,J., Roy,A., Schauer,S., Schupback,R., Seaman,S., Severy,P.,	repeat_region	complement(14619..14992)
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	Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,	repeat_region	complement(15002..17751)
	Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,	repeat_region	/rpt family="L1PB1"
	Zembek,L., Zimmer,A. and Zody,M.	repeat_region	17752..19590
TITLE	Direct Submission	repeat_region	/rpt family="L1PA6"
JOURNAL	Submitted (03-SEP-2002) Whitehead Institute/MIT Center for Genome	repeat_region	19591..20184
	Research, 320 Charles Street, Cambridge, MA 02141, USA	repeat_region	/rpt family="L1PA4"
COMMENT	On Sep 3, 2002 this sequence version replaced gi:22474954.	repeat_region	20185..24476
	All repeats were identified using RepeatMasker:	repeat_region	/rpt family="L1PA6"
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	http://ftp.genome.washington.edu/RM/RepeatMasker.html	repeat_region	/rpt family="(T)n"
	----- Genome Center	repeat_region	complement(24639..26213)
	Center: Whitehead Institute/ MIT Center for Genome Research	repeat_region	/rpt family="SVA"
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	Web site: http://www-seq.wi.mit.edu	repeat_region	/rpt family="L1MB5"
	Contact: sequence submissions@genome.wi.mit.edu	repeat_region	26372..26560
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	Center project name: L24596	repeat_region	complement(26636..26719)
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31198..31246
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repeat_region /rpt family="MIR"
31541..31821
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complement(32650..32747)

Query Match 99.8%; Score 967.4; DB 9; Length 91923;
Best Local Similarity 99.9%; Pred. No. 6.8e-244;
Matches 968; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 10
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DEFINITION
Sequence 1 from Patent WO03080659.
ACCESSION
AX923125
VERSION
AX923125.1 GI:40216228
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1
Peri, K.G., Moffett S. and Abtan, D.
Methods and compounds for prevention and treatment of elevated
intraocular pressure and related conditions
Patent: WO 03080659-A 1 02-OCT-2003;
THERATECHNOLOGIES INC. (CA)
LOCATION/Qualifiers
1. 969

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ORIGIN

Query Match 99.7%; Score 965.8; DB 6; Length 969;
Best Local Similarity 99.8%; Pred. No. 7e-244;
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ACCESSION AF474987
VERSION AF474987.2 GI:31747894
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Lembo, P.M., Grazzini, E., Groblewski, T., O'Donnell, D., Roy, M.-O.,
Zhang, J., Hoffert, C., Cao, J., Schmidt, R., Pelletier, M., Labarre, M.,
Gosselin, M., Fortin, Y., Banville, D., Shen, S., Strom, P., Payza, K.,
Dray, A., Walker, P., and Ahmad, S.
TITLE Proenkephalin A gene products activate a new family of sensory
neuron-specific GPCRs
JOURNAL Nat. Neurosci. 5 (3), 201-209 (2002)
MEDLINE 21853733
PUBMED 11850634
REFERENCE
AUTHORS Ahmad, S., Banville, D., Fortin, Y., Lembo, P.M. and O'Donnell, D.
Direct Submission
TITLE Submitted (25-JAN-2002) Molecular Biology, AstraZeneca, 7171
Frederick-Banting, Montreal, Quebec H4S 1Z9, Canada
COMMENT On Jun 16, 2003 this sequence version replaced gi:19338907.
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Best Local Similarity 99.5%; Pred. No. 1.3e-242;
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961 GAGCAGTGA 969
961 GAGCAGTGA 969
Db
RESULT 14
BD103571
LOCUS
DEFINITION Novel G protein-coupling receptor.
ACCESSION BD103571
VERSION BD103571.1 GI:22649145
KEYWORDS JP 2001526064-A/2.
SOURCE unidentified
ORGANISM unclassified
REFERENCE 1 (bases 1 to 969)
AUTHORS Ahmad, S., Banville, D., Fortin, Y., Lembo, P., O'Donnell, D. and Shen, S.H.
TITLE Novel G protein-coupling receptor
JOURNAL Patent: JP 2001526064-A 2 18-DEC-2001;
ASTRAZENECA CANADA INC
COMMENT
OS Unidentified
PN JP 2001526064-A/2
PD 18-DEC-2001
PF 16-DEC-1998 JP 2000525456
PR 22-DEC-1997 SE 9704836-7
PI SULTAN AHMAD, DENIS BANVILLE, YVES FORTIN, PAOLA LEMBO, DAJAN PI O'DONELL,
PI SHI HSIANG SHEN
PC
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C12N15/09, C07K14/72, C07K16/28, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
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Strandedness: Double;
CC Topology: Linear;
CC Novel G protein-coupling receptor
FH Key Location/Qualifiers
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    Best Local Similarity 98.8%; Pred. No. 1.2e-239; Indels 0; Gaps 0;
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DB 121 GCCTGACAGAAACGGGTGTGCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
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DB 841 CGTCAAAATAGGACAAACCTGAGCTGTTCTCAAGGCTCTGCGAGACACGCTGAG 900
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DB 901 GTGGATGAAGCTGGAGGCTGCTTCTCAGGAAACCTGAGCTGTCGGAAACAGATTG 960
QY 961 GAGCAGTGA 969
DB 961 GAGCAGTGA 969
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AF474988 969 bp DNA linear PRI 16-JUN-2003
LOCUS Homo sapiens G protein-coupled receptor SNR2 gene, complete cds.
DEFINITION AF474988
ACCESSION AF474988
VERSION AF474988.2 GI:31747896
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 969)
AUTHORS Lembo, P.M., Grazzini, E., Groblewski, T., O'Donnell, D., Roy, M.-O.,
Zhang, J., Hoffert, C., Cao, J., Schmidt, R., Pelletier, M., Labarre, M.,
Gosselin, M., Fortin, Y., Banville, D., Shen, S., Strom, P., Payza, K.,
Dray, A., Walker, P. and Ahmad, S.
PROTEIN Phe196
TITLE Proenkephalin A gene products activate a new family of sensory
neuron-specific GPCRs
JOURNAL Nat. Neurosci. 5 (3), 201-209 (2002)
MEDLINE 21853733
PUBMED 11850634
REFERENCE 2 (bases 1 to 969)
AUTHORS Ahmad, S., Banville, D., Fortin, Y., Lembo, P.M. and O'Donnell, D.
DIRECT SUBMISSION
TITLE Submitted (25-JAN-2002) Molecular Biology, Astrazeneca, 7171
JOURNAL Frederick-Banting, Montreal, Quebec H4S 1Z9, Canada
COMMENT On Jun 16, 2003 this sequence version replaced gi:19338909.
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CDS
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ORIGIN

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Query Match 97.5%; Score 945; DB 9; Length 969;
Best Local Similarity 98.5%; Pred. No. 2.2e-238;
Matches 954; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
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Db      |||||
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Db      |||||
961  GAGCAGTGA 969
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Search completed: July 4, 2004, 06:30:03
Job time : 4170 secs

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	Score	Match	Length			
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3	969	100.0	1400	6	AAa33751	Human Mrq
4	969	100.0	1400	7	ABa42395	Human G p
5	969	100.0	2618	6	ABX52852	CDNA enco
6	969	100.0	8622	3	ABX52823	Genomic D
7	967.4	99.8	969	3	AAa29812	Human G p
8	965.8	99.7	1369	9	ADCB6820	Human GPC
9	964.2	99.5	969	3	AAa70342	Human nov
10	949.8	98.0	969	2	AAZ10057	Human dor
11	938.6	96.3	969	2	AAZ10058	Human dor
12	845.8	87.3	909	7	ACC44771	Human G p
13	837.8	86.5	969	3	AAa12208	Human G p
14	837.8	86.5	969	9	ADCL17729	Human TGR
15	836.2	86.3	969	2	AAa10071	Human G p
16	834.6	86.1	969	3	AAa12205	Human G p
17	834.6	86.1	969	9	ADCL17725	Human TGR
18	833	86.0	969	2	AAZ10069	Human dor
19	833	86.0	969	3	AAa12204	Human G p
20	833	86.0	969	6	ABT04874	Human G p
21	833	86.0	969	7	ACC44768	Human G p
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ID	AAI29811 standard; cDNA; 969 BP.
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AC	AAA29811;
XX	
DT	18-AUG-2000 (first entry)
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XX	Human G protein-coupled receptor hHIRT213 encoding cDNA SEQ ID NO:3.
XX	
KW	Human; G protein-coupled receptor; hippocampus; diagnosis; screening;
XX	genetic disease; cellular function regulation; ss.
KW	
OS	Homo sapiens.
XX	
Key	Location/Qualifiers
FT	1..969
CDS	/*tag= a
FT	/products "G protein-coupled receptor"
FT	

XX	Human-derived G protein-coupled protein and encoding nucleic acid, useful
PT	e.g. in determining ligands and treatment of diseases associated with
PT	dysfunction of the protein.
XX	Claim 6; Page 93-94; 97pp; Japanese.
PS	
XX	
XX	The present sequence encodes a human-derived G protein-coupled protein
CC	designated hH17213, which is isolated from the human hippocampus. The G
CC	protein-coupled receptor can be used for preventing, treating and
CC	diagnosing genetic diseases associated with G protein-coupled protein,
CC	and for regulating cellular functions. The protein can be used to prevent
CC	

CC and treat disorders associated with G protein-coupled protein gene
CC dysfunction. It can also be used to identify G protein-coupled protein
CC ligands and generating antibodies and antisera against the protein. It is
CC also useful in constructing recombinant receptor protein expression
CC systems, developing receptor-binding assay systems and screening drug
CC candidates, and can be used as a probe in the genetic diagnosis of G
CC protein-coupled protein disorders
XX
SQ Sequence 969 BP; 171 A; 280 C; 250 G; 268 T; 0 U; 0 Other;

Query Match 100.0%; Score 969; DB 3; Length 969;
Best Local Similarity 100.0%; Pred. No. 7.3e-263;
Matches 969; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 721 AGGATCCACCTGGATTGAAAGTCTTATTTGTCATGTGATCTAGTTTCCATTTTCCCTG 780
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DB 901 GTGGATCAAGTGGAGGGTGGCTTCTCCTCAGGAACCTCGAGCTGTGCGGAACGAGATTG 960
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ID ABT04875 standard; cDNA; 969 BP.
XX ABT04875;
AC AC
XX 11-OCT-2002 (first entry)
DT DT
XX Human G protein coupled receptor hRUP37 coding sequence.
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KW hRUP32; hRUP33; hRUP34; hRUP35; hRUP36; hRUP37; gene; ss.
XX Homo sapiens.
OS WO200242461-A2.
PN 30-MAY-2002.
XX 26-NOV-2001; 2001WO-US044386.
PR 27-NOV-2000; 2000US-0253404P.
PR 12-DEC-2000; 2000US-0255366P.
PR 20-FEB-2001; 2001US-0270286P.
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PR 06-APR-2001; 2001US-0282356P.
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PR 14-MAY-2001; 2001US-0290917P.
PR 31-JUL-2001; 2001US-0309208P.
XX (AREN-) ARENA PHARM INC.
XX Chen R, Chu ZL, Dang HT, Lowitz KP, Pride C;
XX WPI: 2002-566565/50.
XX P-PSDB; ABC04077.
PT Novel endogenous and non-endogenous versions of G protein-coupled
PT receptor useful for identification of candidate compounds as receptor
PT agonists or antagonists for use as therapeutic agents.
XX Claim 39; Page 74; 84pp; English.
XX The present invention provides the protein and coding sequences of
XX several human G-protein coupled receptors (GPCRs). These can be used in
XX the identification of candidate compounds as receptor agonists or inverse
XX agonists having applicability as therapeutic agents. The present sequence
XX is a GPCR coding sequence of the invention
SQ Sequence 969 BP; 171 A; 280 C; 250 G; 268 T; 0 U; 0 Other;

Query Match 100.0%; Score 969; DB 6; Length 969;
Best Local Similarity 100.0%; Pred. No. 7.3e-263;
Matches 969; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGATTCAACCATCCCACTGTTGGGTACAGAACTGACACCAATCAACGGAGCTGAGGAG 60
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Db 872 ATGCGCTGTCCTGTCCTGTCGCGCCATCTGTTACACCTGCGCGCCGCCAGATACCTGTCATCG 931
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Db 1232 GTGATGAGAGTCGTCGTCGCGCCATCTGTTACACCTGCGCGCCGCCAGATACCTGTCATCG 1291
QY 961 GAGCAGTGA 969
Db 1292 GAGCAGTGA 1300

RESULT 4
ID ABZ42595
XX ABZ42595 standard; DNA; 1400 BP.
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XX AC ABZ42595;
XX DT 04-MAR-2003 (first entry)
XX DE Human G protein-coupled receptor Mrx3 nucleotide SEQ ID NO:673.
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XX KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW G protein-coupled receptor modulator; antibody; immune-related disease;
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW immunological-related cell proliferative disease; autoimmune disease;
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KW ulcer; gene; ds.
XX OS Homo sapiens.
XX PN WO200261087-A2.
XX PD 08-AUG-2002.
XX

PF 19-DEC-2001; 2001WO-US050107.
XX 19-DEC-2000; 2000US-0257144P.
XX (LIFE-) LIFESPAN BIOSCIENCES INC.
XX Burmer GC, Roush CL, Brown JP;
XX
XX WPI: 2003-046718/04.
XX P-PSDB; ABP81750.
XX
XX New isolated antigenic peptides e.g., for G protein-coupled receptors
XX (GPCR), useful for diagnosing and designing drugs for treating conditions
XX in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
XX autoimmune diseases.
XX
XX Disclosure; Fig 1; 523pp; English.
XX
XX The present invention describes antigenic peptides (I) comprising: (a)
XX any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
XX acids. Also described: (1) an assay for the detection of a particular G
XX protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
XX and (2) an isolated antibody having high specificity and high affinity or
XX avidity for a particular GPCR. (I) can be used as GPCR modulators and in
XX gene therapy. The antigenic peptides for GPCRs are useful in detecting an
XX antibody against a particular GPCR, and in the production of specific
XX antibodies. The peptides and antibodies are also useful for detecting the
XX presence or absence of corresponding GPCRs. The antigenic peptides for
XX GPCRs and antibodies are useful for diagnosing and designing drugs for
XX treating immune-related diseases, growth-related diseases, cell
XX regeneration-related disease, immunological-related cell proliferative
XX diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
XX atherosclerosis, bacterial, fungal, protozoan or viral infections,
XX osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
XX inflammation, allergies, Crohn's disease, diabetes, pain, psoriasis,
XX disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
XX anxiety, depression, schizophrenia, dementia, mental retardation, memory
XX loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
XX hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
XX any other disorder in which GPCRs are involved. The antibodies may be
XX used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
XX GPCR proteins given in ABP81675 to ABP82018, which are used in the
XX exemplification of the present invention
XX
XX SQ Sequence 1400 BP; 276 A; 375 C; 363 G; 386 T; 0 U; 0 Other;
Query Match 100.0%; Score 969; DB 7; Length 1400;
Best Local Similarity 100.0%; Pred. No. 8.7e-263; Indels 0; Gaps 0;
Matches 969; Conservative 0; Mismatches 0;
QY 1 ATGGATTCAACCATCCAGTCTTGGGTACAGAACTGACCAATCAACGACGTGAGAG 60
Db 332 ATGGATTCAACCATCCAGTCTTGGGTACAGAACTGACCAATCAACGACGTGAGAG 391
QY 61 ACTCCTTCTACAGCAGACCTGAGCTTACGGGGCTGAGCTGATCTTCCCTTGTGTC 120
Db 392 ACTCCTTCTACAGCAGACCTGAGCTTACGGGGCTGAGCTGATCTTCCCTTGTGTC 451
QY 121 GCGCTGACAGAAACCGCGTTGTCTTGGCTCTCTGGGCTCCCGCATGCGCAGAAAGCT 180
Db 452 GCGCTGACAGAAACCGCGTTGTCTTGGCTCTCTGGGCTCCCGCATGCGCAGAAAGCT 511
QY 181 GTCTCCATCTACATCTCAACCTGGTGGCGCCAGATCTTCTTCTAGGGGACATTT 240
Db 512 GTCTCCATCTACATCTCAACCTGGTGGCGCCAGATCTTCTTCTTCTAGGGGACATTT 571
QY 241 ATATGTTGCGGTTACGCTCATCAATATCCGCTCATCTCCAAATCTCAGTCTCT 300
Db 572 ATATGTTGCGGTTACGCTCATCAATATCCGCTCATCTCCAAATCTCAGTCTCT 631
QY 301 GTGATGACCTTCTCCTTACTTTATAGGCTTAAGCATGCTGAGGCGCATCAGACCGAGCGC 360
Db 632 GTGATGACCTTCTCCTTACTTTATAGGCTTAAGCATGCTGAGGCGCATCAGACCGAGCGC 691

QY	361	TGCTGTCCATCTGTGGCCCATCTGTGTACACACTGCCGCGCCAGATACCTGTCTATCG	420
Db	692	TGCTGTCCATCTGTGGCCCATCTGTGTACACACTGCCGCGCCAGATACCTGTCTATCG	751
QY	421	GTCAATGTGTCTCTGTCTCTGGGCCCTGTCCCTGCTGCGGAGTAGTACCTCGAGTGGATGTC	480
Db	752	GTCAATGTGTCTCTGTCTCTGGGCCCTGTCCCTGCTGCGGAGTAGTACCTCGAGTGGATGTC	811
QY	481	TGTGACTTCTCTTTAGTGTGTCTGATCTGTTTGGTGTGAACAGTCAGATTTCAITACA	540
Db	812	TGTGACTTCTCTTTAGTGTGTCTGATCTGTTTGGTGTGAACAGTCAGATTTCAITACA	871
QY	541	ATCCGCTGGCTGTGTTTTTTTATGTGTGGTTCTCTGTGGGTCCAGCCTGGTCTGCTGGTC	600
Db	872	ATCCGCTGGCTGTGTTTTTTTATGTGTGGTTCTCTGTGGGTCCAGCCTGGTCTGCTGGTC	931
QY	601	AGGATTCTCTGTGGATCCCGAGATCCGCTGACACAGGCTGTACGTGACCATCTCTCCTC	660
Db	932	AGGATTCTCTGTGGATCCCGAGATCCGCTGACACAGGCTGTACGTGACCATCTCTCCTC	991
QY	661	ACAGTGTGTCTTTCCTCTCTGTGGCTCGCCCTTTGGCATTCAGTGGGGCCCTGTCTTTC	720
Db	992	ACAGTGTGTCTTTCCTCTCTGTGGCTCGCCCTTTGGCATTCAGTGGGGCCCTGTCTTTC	1051
QY	721	AGGATCCACCTGGATTGGAAAGTCTTATTTGTCACTGCACTAGTATTTCCATTTTCTTG	780
Db	1052	AGGATCCACCTGGATTGGAAAGTCTTATTTGTCACTGCACTAGTATTTCCATTTTCTTG	1111
QY	781	TCCGCTCTTAACAGCAGTGGCAACCCCATCATTTACTTCTTCGTGGGCTCCTTTAGGCAG	840
Db	1112	TCCGCTCTTAACAGCAGTGGCAACCCCATCATTTACTTCTTCGTGGGCTCCTTTAGGCAG	1171
QY	841	CGTCARATAGGCAGAACCTGAAGCTGGTTCTCCAGAGGGCTCTGCAGGACACGCTTGG	900
Db	1172	CGTCARATAGGCAGAACCTGAAGCTGGTTCTCCAGAGGGCTCTGCAGGACACGCTTGG	1231
QY	901	GTGGATGAAGTGGAGGGTGTCTTCTCAGGAAACCTTGGAGCTGTCTGGGAAGCAGATTG	960
Db	1232	GTGGATGAAGTGGAGGGTGTCTTCTCAGGAAACCTTGGAGCTGTCTGGGAAGCAGATTG	1291
QY	961	GAGCAGTGA 969	
Db	1292	GAGCAGTGA 1300	
RESULT 5			
ABK52822			
ID	ABK52822 standard; cDNA; 2618 BP.		
XX			
AC	ABK52822;		
XX			
DT	27-AUG-2002 (first entry)		
XX			
DE	cDNA encoding human G-protein coupled receptor (GPCR).		
XX			
KW	Human; G-protein coupled; receptor; GPCR; human protease;		
KW	human therapeutic protein; query sequence; search; gene; ss;		
KW	sequence database; non-human transgenic animal; gene therapy;		
KW	chromosome 3.		
OS	Homo sapiens.		
OS			
XX			
FH	Key Location/Qualifiers		
CDS	447..1460		
FT	/*tag= a		
FT	/product= "Human G-protein coupled receptor (GPCR) "		
XX			
PN	WO200234914-A1.		
XX			
PD	02-MAY-2002.		
XX			
XP	10-OCT-2001; 2001WO-US031592.		

Db	8068	TGTGACTTCTCTGTTTAGTGGTGTGATCTCTGTTTGGTGTGAACAGTCAGATTTTCATTACA	8067
Qy	541	ATCCGCTGGCTGCTGTTTATGTTGGTTCCTCTGTTGGGTCCAGCCCTGGTCTGCTGGTC	600
Db	8068	ATCCGCTGGCTGCTGTTTATGTTGGTTCCTCTGTTGGGTCCAGCCCTGGTCTGCTGGTC	8127
Qy	601	AGGATTCTCTGTGGATCCCGGAAGATGCCGCTGACCAGGCTGTACGTGACCATCTCCTC	660
Db	8128	AGGATTCTCTGTGGATCCCGGAAGATGCCGCTGACCAGGCTGTACGTGACCATCTCCTC	8187
Qy	661	ACAGTCTGCTTTCCTCTCTGTGGGCTGCCCTTTGGCATTCAGTGGGCCCTGTTTTC	720
Db	8188	ACAGTCTGCTTTCCTCTCTGTGGGCTGCCCTTTGGCATTCAGTGGGCCCTGTTTTC	8247
Qy	721	AGGATCCACCTGGATTCGAAAGCTTATTTGTCACTGTCATCTAGTTCATTTTCCATTTCCTG	780
Db	8248	AGGATCCACCTGGATTCGAAAGCTTATTTGTCACTGTCATCTAGTTCATTTTCCATTTCCTG	8307
Qy	781	TCCGCTCTTAAACAGCAGTGCACCCCATCATTTACTTCTTCGPGGCTCTCTTTAGGCAG	840
Db	8308	TCCGCTCTTAAACAGCAGTGCACCCCATCATTTACTTCTTCGPGGCTCTCTTTAGGCAG	8367
Qy	841	CGTCAAAATAGGCAGAACCTTGAAGCTGGTTCTCCAGAGGGCTCTGACGGACACGCCCTGAG	900
Db	8368	CGTCAAAATAGGCAGAACCTTGAAGCTGGTTCTCCAGAGGGCTCTGACGGACACGCCCTGAG	8427
Qy	901	GTGGATGAAGGTGGAGGGTGCTTCTCAGAAACCTTGAGCTGTGCGGAGCTGTGCGGAAGCAGATTG	960
Db	8428	GTGGATGAAGGTGGAGGGTGCTTCTCAGAAACCTTGAGCTGTGCGGAGCTGTGCGGAAGCAGATTG	8487
Qy	961	GAGCAGTGA 969	
Db	8488	GAGCAGTGA 8496	
RESULT 7			
AAA29812			
ID AAA29812 standard; cDNA; 969 BP.			
XX	AC	AAA29812;	
XX	DT	18-AUG-2000 (first entry)	
XX	DE	Human G protein-coupled receptor hH17T213V encoding cDNA SEQ ID NO:4.	
KW	KW	Human; G protein-coupled receptor; hippocampus; diagnosis; screening; genetic disease; cellular function regulation; ss.	
KW	OS	Homo sapiens.	
XX	Key	Location/Qualifiers	
XX	CDS	1..969	
FT	FT	/*tag= a	
FT	FT	/product= "G protein-coupled receptor"	
XX	XX		
XX	XX	WO200020455-A1.	
XX	XX	13-APR-2000.	
XX	XX	30-SEP-1999; 99WO-JP005366.	
XX	XX	01-OCT-1998; 98JP-00279535.	
XX	XX	(TAKE) TAKEDA CHEM IND LTD.	
XX	XX	Watanabe T, Terao Y, Matsui H;	
XX	XX	WPI; 2000-303747/26.	
XX	XX	P-PSDB; AAY90762.	

XX Human-derived G protein-coupled protein and encoding nucleic acid, useful
PT e.g. in determining ligands and treatment of diseases associated with
PT dysfunction of the protein.

XX Claim 6; Page 94-95; 97pp; Japanese.
 XX The present sequence encodes a human-derived G protein-coupled protein
 CC designated hN17213V, which is isolated from the human hippocampus. The G
 CC protein-coupled receptor can be used for preventing, treating and
 CC diagnosing genetic diseases associated with G protein-coupled protein,
 CC and for regulating cellular functions. The protein can be used to prevent
 CC and treat disorders associated with G protein-coupled protein gene
 CC dysfunction. It can also be used to identify G protein-coupled protein
 CC ligands and generating antibodies and antisera against the protein. It is
 CC also useful in constructing recombinant receptor protein expression
 CC systems, developing receptor-binding assay systems and screening drug
 CC candidates, and can be used as a probe in the genetic diagnosis of G
 CC protein-coupled protein disorders
 XX
 SQ Sequence 969 BP; 172 A; 280 C; 249 G; 268 T; 0 U; 0 Other;

 Query Match 99.8%; Score 967.4; DB 3; Length 969;
 Best Local Similarity 99.9%; Pred. No. 2.1e-262;
 Matches 968; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

 QY 1 ATGATTCAACCATCCAGCTTTGGGTACAGAACTGACACCAATCAACGGACGTGAGAG 60
 DB 1 ATGATTCAACCATCCAGCTTTGGGTACAGAACTGACACCAATCAACGGACGTGAGAG 60

 QY 61 ACTCTTTGTACAGCAGACCTTGAGCTTCACGGGGCTGAGTGCATCTGTTCCCTGTC 120
 DB 61 ACTCTTTGTACAGCAGACCTTGAGCTTCACGGGGCTGAGTGCATCTGTTCCCTGTC 120

 QY 121 GCGCTGACAGAAACGGGGTTGTCTCTGGCTCTGGGCTGCCCATGCGCAGAAACGCT 180
 DB 121 GCGCTGACAGAAACGGGGTTGTCTCTGGCTCTGGGCTGCCCATGCGCAGAAACGCT 180

 QY 181 GTCTCCTATACATCTTCACTGGTGGCGGCGACCTCTCTTCTTAGCGGCACATT 240
 DB 181 GTCTCCTATACATCTTCACTGGTGGCGGCGACCTCTCTTCTTAGCGGCACATT 240

 QY 241 ATATGTTTCGGCGTTACGCTCATCAATATCGGCATCCCATCTCCAAAATCCTCAGTCCT 300
 DB 241 ATATGTTTCGGCGTTACGCTCATCAATATCGGCATCCCATCTCCAAAATCCTCAGTCCT 300

 QY 301 GTGATGACCTTTCCTACTTATAGGCTTAGCATGTGAGCGGCATCAGCACCGAGCGC 360
 DB 301 GTGATGACCTTTCCTACTTATAGGCTTAGCATGTGAGCGGCATCAGCACCGAGCGC 360

 QY 361 TGCCTGTCCATCTGTGGCCCATCTGTAACACTTGCCTGCCCGCCCCAGATCCTGTATCG 420
 DB 361 TGCCTGTCCATCTGTGGCCCATCTGTAACACTTGCCTGCCCGCCCCAGATCCTGTATCG 420

 QY 421 GTCATGTGTCTGCTCTGGGCGCTGTCCTGTCTGGGAGTATCTGAGTGGATGTC 480
 DB 421 GTCATGTGTCTGCTCTGGGCGCTGTCCTGTCTGGGAGTATCTGAGTGGATGTC 480

 QY 481 TGTGACCTTCCTGTTAGTGGTGTCTGTTTGGTGTGAACGTCAGATTCATTACA 540
 DB 481 TGTGACCTTCCTGTTAGTGGTGTCTGTTTGGTGTGAACGTCAGATTCATTACA 540

 QY 541 ATCCGCTGGCTGGTTTTTTATGTGTGTTCTCTGTGGGTCCAGCTGGTCTGCTGTC 600
 DB 541 ATCCGCTGGCTGGTTTTTTATGTGTGTTCTCTGTGGGTCCAGCTGGTCTGCTGTC 600

 QY 601 AGGATTCCTCTGGATCCCGAAGATGCCGTGACCGAGCTGTAGTCAACCATCCTCCTC 660
 DB 601 AGGATTCCTCTGGATCCCGAAGATGCCGTGACCGAGCTGTAGTCAACCATCCTCCTC 660

 QY 661 ACAGTGTGTCTTCCCTCTGTGGCTGCCCTTTGGCATTCAGTGGGCCCTGTTTCC 720
 DB 661 ACAGTGTGTCTTCCCTCTGTGGCTGCCCTTTGGCATTCAGTGGGCCCTGTTTCC 720

 QY 721 AGGATCCACCTGGATTGAAAGTCTTATTTGTGATGTGATCTAGTTTCAATTTCTCTG 780
 DB 721 AGGATCCACCTGGATTGAAAGTCTTATTTGTGATGTGATCTAGTTTCAATTTCTCTG 780

QY 781 TCCGCTCTTAACAGCAGTGCACACCCCATCAATTACTTCTTCGTGGGTCCTTTAGGCAG 840
Db 781 TCCGCTCTTAACAGCAGTGCACACCCCATCAATTACTTCTTCGTGGGTCCTTTAGGCAG 840
QY 841 CGTCAAAATAGGCAGAACCTGAAGCTGTCTCCAGAGGCTCTGAGGACACGCTGAG 900
Db 841 CGTCAAAATAGGCAGAACCTGAAGCTGTCTCCAGAGGCTCTGAGGACACGCTGAG 900
QY 901 GTGATGAAGTGGAGGGTGGCTCTCAGGAACCCCTGAGCTGTCCGGAGCAGATTG 960
Db 901 GTGATGAAGTGGAGGGTGGCTCTCAGGAACCCCTGAGCTGTCCGGAGCAGATTG 960
QY 961 GAGCAGTGA 969
Db 961 GAGCAGTGA 969

RESULT 8

ADC86820
ID ADC86820 standard; DNA; 1369 BP.

XX AC ADC86820;

XX 01-JAN-2004 (first entry)

DT Human GPCR gene SEQ ID NO:1273.

XX ds; gene; human; GPCR;

KW Guanosine triphosphate-binding protein coupled receptor; gene therapy.

XX Homo sapiens.

XX EP1270724-A2.

XX 02-JAN-2003.

XX 18-JUN-2002; 2002EP-00013517.

XX 18-JUN-2001; 2001JP-00246789.

XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.

XX (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.

XX Suwa M, Asai K, Akiyama Y, Aburatani H;

XX WPI; 2003-315783/31.

XX P-PSDB; ADC86821.

XX New polynucleotide, useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the guanosine triphosphate-binding protein coupled receptor.

PS Claim 1; SEQ ID NO 1273; 28pp; English.

CC The invention relates to a novel polynucleotide encoding a guanosine triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of the invention may have a use in gene therapy. The polynucleotide and polypeptide are useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the guanosine triphosphate-binding protein coupled receptor. The polynucleotide sequences shown in ADC85548-ADC87616 encode GPCR's of the invention.

SQ Sequence 1369 BP; 272 A; 372 C; 340 G; 385 T; 0 U; 0 Other;

Query Match 99.7%; Score 965.8; DB 9; Length 1369;

Best Local Similarity 99.8%; Pred. No. 6.9e-262;

Matches 967; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGATTCAACCATCCAGCTTGGGTACAGAACTGACACCAATCAAGCGAGTGGAG 60

Db 201 ATGGATTCAACCATCCAGCTTGGGTACAGAACTGACACCAATCAAGCGAGTGGAG 260

QY 61 ACTCTTCTCTAAGCAGAACCTCAGCTTCAOGGGCTGACGTGCATCGTTTCCCTGTGC 120
Db 261 ACTCTTCTCTAAGCAGAACCTCAGCTTCAOGGGCTGACGTGCATCGTTTCCCTGTGC 320
QY 121 GGGCTGACAGAAACCGGTTGTCTCTGGCTCCTCGGGCTGCCGATCGCCAGAAACGCT 180
Db 321 GGGCTGACAGAAACCGGTTGTCTCTGGCTCCTCGGGCTGCCGATCGCCAGAAACGCT 380
QY 181 GTCTCATCTACATCTCAACCTGGTGGCGGCGACACTTCTCTCTTCTTAGCGGCACATT 240
Db 381 GTCTCATCTACATCTCAACCTGGTGGCGGCGACACTTCTCTCTTCTTAGCGGCACATT 440
QY 241 ATATGTTGGCGGTTACGGCTCATCAATATCCGCCATCCCATCTCCAAAATCTCAGTCTCT 300
Db 441 ATATGTTGGCGGTTACGGCTCATCAATATCCGCCATCCCATCTCCAAAATCTCAGTCTCT 500
QY 301 GTGATGACCTTTCCTACTTTATAGGCTAAGCATGTGAGCGCCATCAGACCGAGCGC 360
Db 501 GTGATGACCTTTCCTACTTTATAGGCTAAGCATGTGAGCGCCATCAGACCGAGCGC 560
QY 361 TGCCTGTCCATCTGTGGCCCATCTGTACACATGCCCGCCGCCCCAGATACCTGTCTATCG 420
Db 561 TGCCTGTCCATCTGTGGCCCATCTGTACACATGCCCGCCGCCCCAGATACCTGTCTATCG 620
QY 421 GTCATGTGTCTCTGCTCTGGGCGCTGTCCCTGTGGGAGTATCCTGGAGTGGATGTTTC 480
Db 621 GTCATGTGTCTCTGCTCTGGGCGCTGTCCCTGTGGGAGTATCCTGGAGTGGATGTTTC 680
QY 481 TGTGACTTCCCTGTTTAGTGTGCTGATCTGTGTTGGTGAAACGTCAGATTCATTACA 540
Db 681 TGTGACTTCCCTGTTTAGTGTGCTGATCTGTGTTGGTGAAACGTCAGATTCATTACA 740
QY 541 ATCGCGTGGCTGTTTATGTTGTTCTCTGTGGGTCCAGCCCTGGTCTGCTGGTGC 600
Db 741 ATCGCGTGGCTGTTTATGTTGTTCTCTGTGGGTCCAGCCCTGGTCTGCTGGTGC 800
QY 601 AGGATCTCTGTGATGCCGGAAGATCCCGTACAGGCTGTACGTGACCATCTCTCTC 660
Db 801 AGGATCTCTGTGATGCCGGAAGATCCCGTACAGGCTGTACGTGACCATCTCTCTC 860
QY 661 ACAGTGTCTGCT 720
Db 861 ACAGTGTCTGCT 920
QY 721 AGGATCCACCTGGATGGAAAGTCTTATTTGTCATGTGCATGTAGTTCATTTCCCTG 780
Db 921 AGGATCCACCTGGATGGAAAGTCTTATTTGTCATGTGCATGTAGTTCATTTCCCTG 980
QY 781 TCCGCTCTTAACAGCAGTGCACACCCCATCATTTACTTCTTCGTGGGCTCCTTTAGGCAG 840
Db 981 TCCGCTCTTAACAGCAGTGCACACCCCATCATTTACTTCTTCGTGGGCTCCTTTAGGCAG 1040
QY 841 CGTCAAAATAGGCAGAACCTCAGCTGTTCTCCAGAGGCTCTGAGGACACGCTGAG 900
Db 1041 CGTCAAAATAGGCAGAACCTCAGCTGTTCTCCAGAGGCTCTGAGGACACGCTGAG 1100
QY 901 GTGGATGAAGTGGAGGTGGCTTCTCAGAAACCTCGAGCTGTGCGGAGACAGATTG 960
Db 1101 GTGGATGAAGTGGAGGTGGCTTCTCAGAAACCTCGAGCTGTGCGGAGACAGATTG 1160
QY 961 GAGCAGTGA 969
Db 1161 GAGCAGTGA 1169

RESULT 9

AAA70342

ID AAA70342 standard; cDNA; 969 BP.

XX AC AAA70342;

XX AC AAA70342;

DT 19-DEC-2000 (first entry)

XX DE Human novel G-protein coupled receptor #1 coding sequence.
 XX DE Human; novel G-protein coupled receptor; signal transduction;
 KW disease diagnosis; drug screening; disease therapy; ss.
 XX OS Homo sapiens.
 XX Key Location/Qualifiers
 XX CDS 1..969
 XX FT /*tag= a
 XX FT /product= "novel G-protein coupled receptor #1"
 XX PN WO200040724-A1.
 XX PD 13-JUL-2000.
 XX PF 04-JAN-2000; 2000WO-US000052.
 XX PR 04-JAN-1999; 99US-0114666P.
 XX PR 14-JAN-1999; 99US-0115828P.
 XX (LEXI-) LEXICON GENETICS INC.
 XX PA Nehls M, Wattler F;
 XX PI WPI; 2000-465986/40.
 XX DR P-PSDB; AAB14846.
 XX PT New polynucleotides encoding novel G-protein coupled receptors useful for
 PT diagnosis, drug screening, clinical trial monitoring and for the
 PT treatment of physiological or behavioral disorders.
 XX PS Claim 1; Page 52-53; 61pp; English.
 XX CC The present sequence is the coding sequence for a novel human G-protein
 CC coupled receptor (NGPCR). These proteins are involved in signal
 CC transduction pathways in many cases. The protein contains seven
 CC transmembrane domains, and is expressed in human testis, mammary gland
 CC and salivary gland tissue. The gene, its protein, agonists, antagonists
 CC and antibodies can be used to diagnose and treat diseases associated with
 CC the inappropriate expression or expression of mutant versions of the
 CC protein, for screening for drugs which can be used in the same manner,
 CC and for elucidating the function of the protein
 XX SQ Sequence 969 BP; 172 A; 282 C; 249 G; 266 T; 0 U; 0 Other;

Query Match 99.5%; Score 964.2; DB 3; Length 969;
 Best Local Similarity 99.7%; Pred. No. 1.7e-261;
 Matches 966; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGGATTCAACCATCCAGTCTTGGGTACAGAACTGACACCAATCAACGACGTGAGGAG 60
 Db 1 ATGGATTCAACCATCCAGTCTTGGGTACAGAACTGACACCAATCAACGACGTGAGGAG 60
 QY 51 ACTCTTCTCAAGCAGACCCCTGAGCTTACGGGGCTGACGTGATCGTTTCCCTGTC 120
 Db 51 ACTCTTCTCAAGCAGACCCCTGAGCTTACGGGGCTGACGTGATCGTTTCCCTGTC 120
 QY 121 CGGTGACAGGAACCGCGTTGTGCTCTGGCTCTCTGGGCTCCCGCATGCGCAGGAACGCT 180
 Db 121 CGGTGACAGGAACCGCGTTGTGCTCTGGCTCTCTGGGCTCCCGCATGCGCAGGAACGCT 180
 QY 181 GTCTCCATCTACATCTCAACTGGTTCGGCGCGACATCTCTTCTTAGGGCCACATT 240
 Db 181 GTCTCCATCTACATCTCAACTGGTTCGGCGCGACATCTCTTCTTAGGGCCACATT 240
 QY 241 ATATGTTCCGGTTCACGCTCATCAATATCCGCATCCCATCTCCAAATCTCAGTCCT 300
 Db 241 ATATGTTCCGGTTCACGCTCATCAATATCCGCATCCCATCTCCAAATCTCAGTCCT 300
 QY 301 GTGATGACCTTTCCTACTTTATAGGCTTAAGCAATGCTGAGCGCAATCAGACCGAGGC 360

Db 301 GTGATGACCTTTCCTACTTTATAGGCTTAAGCAATGCTGAGCGCAATCAGACCGAGGC 360
 QY 361 TGCCTGTCCATCTCTGGCCCATCTGTATACCTGCGCGCCGCCCCAGATACCTGTATCG 420
 Db 361 TGCCTGTCCATCTCTGGCCCATCTGTATACCTGCGCGCCGCCCCAGATACCTGTATCG 420
 QY 421 GTCATGTGTGTCCTGCTCTGGCCCTGTCCCTGTGGAGTATCCCTGGAGTGGATGTC 480
 Db 421 GTCATGTGTGTCCTGCTCTGGCCCTGTCCCTGTGGAGTATCCCTGGAGTGGATGTC 480
 QY 481 TGTGACTTCTCTGTTTAGTGGTCTGATCTCTGTTGGTGTGAACGTCAGATTCATTACA 540
 Db 481 TGTGACTTCTCTGTTTAGTGGTCTGATCTCTGTTGGTGTGAACGTCAGATTCATTACA 540
 QY 541 ATCGCGTGGCTGGTTTTTTTATGTGTGGTCTCTGTGGGTCAGGCTGCTCTGCTGTC 600
 Db 541 ATCGCGTGGCTGGTTTTTTTATGTGTGGTCTCTGTGGGTCAGGCTGCTCTGCTGTC 600
 QY 601 AGGATTCTCTGTGGATCCCGGAAGATGCGGTGACAGGCTGTACGTGACCATCTCTCCTC 660
 Db 601 AGGATTCTCTGTGGATCCCGGAAGATGCGGTGACAGGCTGTACGTGACCATCTCTCCTC 660
 QY 661 ACAGTGTGCTGCTCTCTCTCTGTGGCTGCTTGTGCAATTCAGTGGGCTCTGTTTTC 720
 Db 661 ACAGTGTGCTGCTCTCTCTCTGTGGCTGCTTGTGCAATTCAGTGGGCTCTGTTTTC 720
 QY 721 AGGATCCACCTGGATTGGAAGTCTTATTTGTATGTGATCTAGTTTCCATTTTCTG 780
 Db 721 AGGATCCACCTGGATTGGAAGTCTTATTTGTATGTGATCTAGTTTCCATTTTCTG 780
 QY 781 TCCGCTCTTAACAGCAGTGCACCAACCCCATCATTTCTTCTGTTGGGCTCTCTTAGGAG 840
 Db 781 TCCGCTCTTAACAGCAGTGCACCAACCCCATCATTTCTTCTGTTGGGCTCTCTTAGGAG 840
 QY 841 CCTCAAAATAGCAGAACTGAAAGTGTCTTCCAGAGGGCTCTGACGACACGCTGAG 900
 Db 841 CCTCAAAATAGCAGAACTGAAAGTGTCTTCCAGAGGGCTCTGACGACACGCTGAG 900
 QY 901 GTGGATGAAGTGGAGGTGGCTTCTCAGGAACCCCTGGAGCTGTCTGGGAAGCAGATTG 960
 Db 901 GTGGATGAAGTGGAGGTGGAGGTCTTCTCAGGAACCCCTGGAGCTGTCTGGGAAGCAGATTG 960
 QY 961 GAGCAGTGA 969
 Db 961 GAGCAGTGA 969

RESULT 10
 AAZ10067
 ID AAZ10067 standard; DNA; 969 BP.
 XX AAZ10067;
 AC AC
 XX 20-MAR-2003 (revised)
 DT 26-NOV-1999 (first entry)
 XX Human dorsal root receptor 1 hDRR1 nucleotide sequence.
 DE Dorsal root receptor; dorsal root ganglia; G-protein coupled receptor;
 KW hDRR1; central nervous system; CNS; anaesthesia; analgesia; neuron;
 KW pain. ss.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 XX CDS 1..969
 XX FT /*tag= a
 XX FT /product= "hDRR1"
 XX FT /note= "Human dorsal root receptor 1"
 XX PN WO9932519-A1.
 XX PD 01-JUL-1999.

XX 16-DEC-1998; 98WO-SE002348.
 XX 22-DEC-1997; 97SE-00004836.
 XX (ASTR) ASTRA PHARMA INC.
 XX (ASTR) ASTRA AB.
 XX Ahmad S, Banville D, Fortin Y, Lembo P, O'donnell D, Shen S;
 XX WPI; 1999-405162/34.
 XX P-PSDB; AAY30159.
 XX Rat and human dorsal root receptors and related polynucleotides, useful
 XX for identifying agents for anesthesia and analgesia.
 XX Claim 10; Page 42-43; 72pp; English.
 XX This is the human dorsal root receptor 1 (hDRR1) nucleotide sequence.
 CC hDRR1 is a G protein coupled receptor that is expressed preferentially in
 CC dorsal root ganglia. hDRR1 can be used to create antibodies against
 CC hDRR1. The dorsal root ganglia area of the central nervous system (CNS)
 CC is densely innervated with primary or afferent neurons involved in
 CC transmission, modulation and sensation of pain. The DR's which are
 CC expressed in this region of the CNS may be used for assays for the
 CC identification of new agents for anaesthesia and analgesia. (Updated on
 CC 20-MAR-2003 to correct PA field.)
 XX
 XX Sequence 969 BP; 179 A; 283 C; 239 G; 268 T; 0 U; 0 Other;

Query Match 98.0%; Score 949.8; DB 2; Length 969;
 Best Local Similarity 98.8%; Pred. No. 1.9e-257;
 Matches 957; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ATGATTACACACCTCCAGTCTTGGTACAGAACTGACACCAATCAAGGACGTGAGAG 60
 DB 1 ATGATCCACACCTCCAGTCTTGGTACAAACTGACACCAATCAAGGACGTGAGAG 60
 QY 61 ACTCTTGTACAAAGACAGACCTTGAGCTTCAAGGGCTGACGTGATCTTCCCTGTC 120
 DB 61 ACTCTTGTACAAAGACAGACCTTGAGCTTCAAGGGCTGACGTGATCTTCCCTGTC 120
 QY 121 GCGGTACAGAGAAACGGGTGTCCTGCTCTGGCTCCCTGGGTGCGGATCGCAGGAAGCT 180
 DB 121 GCGGTACAGAGAAACGGGTGTCCTGCTCTGGCTCCCTGGGTGCGGATCGCAGGAAGCT 180
 QY 181 GTCTCCATCTACATCTCAACTGTGCTGGGGGAGCTTCTTCTTCTAGCGGCACATT 240
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 QY 241 ATATGTTGCGCGTTAGCGCTCATCAATATCCGCCATCCCATCTCCAAAATCTCAGTCT 300
 DB 241 ATATTTTGGCGTTACCGCTCATCAATATCCGCCATCCCATCTCCAAAATCTCAGTCT 300
 QY 301 GTGATGACCTTCCCTACTTTATAGGCTTAAGCATGCTAGCGCCATCAGCAGCGGC 360
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 QY 361 TGCCTGTCCATCTCTGTGGCCCATCTGTTACCACTGCGCGCCGCCAGATACCTGTCTATCG 420
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 QY 421 GTCATGTGTCCTGCTCGGGCCCTGCTGCTGCTGCGGAGTATCTCGAGTGGATGTC 480
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 QY 541 ATCCGCTGGCTGTTTATGTTGTTGTTCTGTTGGTCCAGCTGGTCTGCTGCTGTC 600
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QY 601 AGGATTCCTGTGGATCCCGAAGATCGCGTACAGAGCTGTACGTGACCATCTCCTC 660
 DB 601 AGGATTCCTGTGGATCCCGAAGATCGCGTACAGAGCTGTACGTGACCATCTCCTC 660
 QY 661 ACAGTGTGCTCTTCTCCTCTGTGGCTGCCCTTTGGCATTCAGTGGGCGCTGTTTCC 720
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 QY 721 AGGATCCACCTGGATTCGAAAGTCTTATTTGTGTCATGTGATCTAGTTCATTTTCC 780
 DB 721 AGGATCCACCTGGATTCGAAAGTCTTATTTGTGTCATGTGATCTAGTTCATTTTCC 780
 QY 781 TCCGCTCTTAACAGACAGTGCACACCCCATCATTTACTTCTTCTGGGCTCCTTTAGG 840
 DB 781 TCCGCTCTTAACAGACAGTGCACACCCCATCATTTACTTCTTCTGGGCTCCTTTAGG 840
 QY 841 CGTCAAAATAGCGAAGACCTGAAGCTGTTCTCCAGAGGCTCTCGAGGACACGCTGAG 900
 DB 841 CGTCAAAATAGCGAAGACCTGAAGCTGTTCTCCAAAGGCTCTCGAGGACACGCTGAG 900
 QY 901 GTGATGAGTGTGAGGCTGCTTCTCAGAAACCTGAGCTGTGCGGAGCAGATTG 960
 DB 901 GTGATGAGTGTGAGGCTGCTTCTCAGAAACCTGAGCTGTGCGGAGCAGATTG 960
 QY 961 GAGCAGTCA 969
 DB 961 GAGCAGTCA 969

RESULT 11

AAZ10068
 ID AAZ10068 standard; DNA; 969 BP.

XX AAZ10068;
 AC
 XX 20-MAR-2003 (revised)
 DT 26-NOV-1999 (first entry)
 XX Human dorsal root receptor 2 hDRR2 nucleotide sequence.
 DE
 XX Dorsal root receptor; dorsal root ganglia; G-protein coupled receptor;
 KW hDRR2; central nervous system; CNS; anaesthesia; analgesia; neuron;
 KW pain. ss.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH 1. .969
 FT /tag= a
 FT /product= "hDRR2"
 FT /note= "Human dorsal root receptor 2"
 XX WO9932519-A1.
 XX 01-JUL-1999.
 PD 16-DEC-1998; 98WO-SE002348.
 PF 22-DEC-1997; 97SE-00004836.
 XX (ASTR) ASTRA PHARMA INC.
 PA (ASTR) ASTRA AB.
 XX Ahmad S, Banville D, Fortin Y, Lembo P, O'donnell D, Shen S;
 XX WPI; 1999-405162/34.
 DR P-PSDB; AAY30160.
 XX Rat and human dorsal root receptors and related polynucleotides, useful
 PT for identifying agents for anesthesia and analgesia.
 XX Claim 15; Page 46-47; 72pp; English.


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QY 361 TGCCTGCTCCATCTCTGGGCCCACTCTGGTACCACTGCCGCCGCCGACAGATACCTGTCTATCG 420
Db 361 TGCCTGCTCTCTCTGGGCCCACTCTGGTACCACTGCCGCCGCCGACAGATACCTGTCTATCG 420
QY 421 GTCATGTGTCTCTCTGGGCCCACTCTGGTACCACTGCCGCCGCCGACAGATACCTGTCTATCG 480
Db 421 GTCATGTGTCTCTCTGGGCCCACTCTGGTACCACTGCCGCCGCCGACAGATACCTGTCTATCG 480
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Db 481 TGTGACTTCTCTCTGGGCCCACTCTGGTACCACTGCCGCCGCCGACAGATACCTGTCTATCG 540
QY 541 ATCGGCTGCTCTCTCTGGGCCCACTCTGGTACCACTGCCGCCGCCGACAGATACCTGTCTATCG 600
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Db 601 AGGATCTCTCTCTGGGCCCACTCTGGTACCACTGCCGCCGCCGACAGATACCTGTCTATCG 660
QY 661 ACAGTGTCTCTCTCTGGGCCCACTCTGGTACCACTGCCGCCGCCGACAGATACCTGTCTATCG 720
Db 661 ACAGTGTCTCTCTCTGGGCCCACTCTGGTACCACTGCCGCCGCCGACAGATACCTGTCTATCG 720
QY 721 AGGATCTCTCTCTGGGCCCACTCTGGTACCACTGCCGCCGCCGACAGATACCTGTCTATCG 780
Db 721 AGGATCTCTCTCTGGGCCCACTCTGGTACCACTGCCGCCGCCGACAGATACCTGTCTATCG 780
QY 781 TCCGCTCTCTCTCTGGGCCCACTCTGGTACCACTGCCGCCGCCGACAGATACCTGTCTATCG 840
Db 781 TCCGCTCTCTCTCTGGGCCCACTCTGGTACCACTGCCGCCGCCGACAGATACCTGTCTATCG 840
QY 841 CTTCAAAATAGCAGAACTCTGAGCTGTTCTCCAGAGGCTCTCCAGGACACGCTCTGAG 900
Db 841 CTTCAAAATAGCAGAACTCTGAGCTGTTCTCCAGAGGCTCTCCAGGACACGCTCTGAG 900
QY 901 GTGGATGAAGTGGAGGCTCTCTGAGGAACTCTGAGGCTCTGAGGCTCTGAGGCTCTGAGGCT 960
Db 901 GTGGATGAAGTGGAGGCTCTCTGAGGAACTCTGAGGCTCTGAGGCTCTGAGGCTCTGAGGCT 960
QY 961 GAGCAGTGA 969
Db 961 GGGCCATGA 969
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RESULT 15

AAZ10071

ID AAZ10071 standard, DNA; 969 BP.

XX AC AAZ10071;

XX XX

DT 20-MAR-2003 (revised)

DT 26-NOV-1999 (first entry)

XX XX

DE Human dorsal root receptor 5 hDRR5 nucleotide sequence.

XX XX

KW Dorsal root receptor; dorsal root ganglia; G-protein coupled receptor;

KW hDRR5; central nervous system; CNS; anaesthesia; analgesia; neuron;

KW pain. ss.

XX XX

OS Homo sapiens.

XX XX

FH Key Location/Qualifiers

FT CDS 1..969

FT /tag= a

FT /note= "hDRR5"

FT /transl_except= (pos:244..246, aa:Cys)

FT /transl_except= (pos:247..249, aa:Arg)

FT /transl_except= (pos:442..444, aa:Ala)

FT /transl_except= (pos:445..447, aa:Gly)

FT /transl_except= (pos:448..450, aa:Leu)

XX WO9932519-A1.

XX PD 01-JUL-1999.

XX XX

XX PF 16-DEC-1998; 98WO-SE002348.

XX XX

XX PR 22-DEC-1997; 97SE-00004836.

XX XX

XX PA (ASTR) ASTRA PHARMA INC.

XX XX

XX PA (ASTR) ASTRA AB.

XX XX

XX PI Ahmad S, Banville D, Fortin Y, Lembo P, O'donnell D, Shen S;

XX XX

XX DR WPI; 1999-405162/34.

XX DR P-PSDB; AAY30363.

XX XX

XX PT Rat and human dorsal root receptors and related polynucleotides, useful

XX PT

XX XX

XX PS for identifying agents for anaesthesia and analgesia.

XX XX

XX XX

XX CC Claim 30; Page 59-60; 72pp; English.

XX CC

XX CC This is the human dorsal root receptor 5 (hDRR5) nucleotide sequence.

XX CC

XX CC hDRR5 is a G protein coupled receptor that is expressed preferentially in

XX CC

XX CC dorsal root ganglia. hDRR5 can be used to create antibodies against

XX CC

XX CC hDRR5. The dorsal root ganglia area of the central nervous system (CNS)

XX CC

XX CC is densely innervated with primary or afferent neurons involved in

XX CC

XX CC transmission, modulation and sensation of pain. The DRG's which are

XX CC

XX CC expressed in this region of the CNS may be used for assays for the

XX CC

XX CC identification of new agents for anaesthesia and analgesia. (Updated on

XX CC

XX CC 20-MAR-2003 to correct PA field.)

XX XX

XX SQ

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Qy	541	ATCCGCTGGCTGGTCTTTTATGTCGTGTCCTCTGTGGTCCAGCCTGGTCTCTGGTCTG	600
Db	541	GTCCGCTGGCTGATTTTTTATGTCGTGTCCTCTGTGGTCCAGCCTGGTCTCTGGTCTG	600
Qy	601	AGGATTCCTCTGTGGATCCCGAAGATGCCGTGACCGAGGCTGTACGTGACCATCCTCCTC	660
Db	601	AGGATCCTCTCTGTGGATCCCGAAGATGCCGTGACCGAGGCTGTATGTGACCATCCTGCTC	660
Qy	661	ACAGTGTGTCCTTCCCTCTGTGGCTGCTGCTTGGCATTCAGTGGGCTGTTTCC	720
Db	661	ACAGTGTGTCCTTCCCTCTGTGGCTGCTGCTTGGCATTCAGTGGGCTGTTTCC	720
Qy	721	AGGATCCACCTGGATTTGAAAGTCTTATTTTGTGATGTGATCTAGTTTCCATTTTCTTG	780
Db	721	AGGATGCACCTGAATTTGGAAGTCTTATTTTGTGATGTGATCTAGTTTCTGATGCTCCTG	780
Qy	781	TCCGCTCTTAACAGCAGTGCCAAACCCATCATTTTACTTCTCTGTGGCTCTTTAGGCAG	840
Db	781	TCCTCTCTAAACAGTAGTGCCAAACCCCATCATTTTACTTCTCTGTGGCTCTTTAGGCAG	840
Qy	841	CGTCAAAATAGGCAGAACCTGAAGTGTCTCCAGAGGGCTCTGCAGGACACGCTGAG	900
Db	841	CGTCAAAATAGGCAGAACCTGAAGTGTCTCCAGAGGGCTCTGCAGGACACGCTGAG	900
Qy	901	GTGGATGAAGTGGAGGGTGGCTTCTCAGGAAACCTTGAGCTGTGCGGAGCAGATTG	960
Db	901	GTGGATAAAGTGAAGGGCAGCTTCTCAGGAAAGCCTTGAGCTGTGCGGAGGAGATTG	960
Qy	961	GAGCAGTGA	969
Db	961	GGGCCATGA	969

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Job time : 482 secs

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OM nucleic - nucleic search, using sw model

Run on: July 4, 2004, 05:08:07 ; Search time 94 Seconds
(without alignments)
5720.717 Million cell updates/sec

Title: US-09-787-879C-3
Perfect score: 969
Sequence: 1 atggattcaaccatccagc.....gaagcagattggagcagtga 969

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	291	30.0	291	4	US-09-495-050A-164
2	275	28.4	275	4	US-09-016-434-330
3	118.6	12.2	1388	4	US-09-016-434-1225
4	118.6	12.2	1388	5	PCT-US93-06251-26
5	110.8	11.4	2435	4	US-09-484-970B-134
6	96.8	10.0	2416	4	US-09-016-434-1264
7	94.2	9.7	1327	6	5320941-1
8	64.4	6.6	1296	4	US-09-016-434-210
9	60.6	6.3	7218	1	US-08-232-463-14
10	59.2	6.1	2911	3	US-08-981-825-5
11	59.2	6.1	2911	3	US-09-480-784-5
12	58.4	6.0	2328	4	US-09-016-434-1188
13	58.4	6.0	2328	4	US-09-023-655-1018
14	51.6	5.3	263	3	US-09-016-434-327
15	51.6	5.3	265	3	US-08-513-974B-337
16	50	5.2	283	4	US-09-016-434-489
17	49.4	5.1	1002	4	US-09-170-496D-7
18	49.4	5.1	1002	4	US-09-170-496D-167
19	49.4	5.1	1265	4	US-09-016-434-1430
20	48.2	5.0	1866	4	US-09-016-434-1205
21	47.8	4.9	1285	3	US-09-016-434-1366
22	47.6	4.9	1875	3	US-09-422-869-21
23	47.6	4.9	49136	3	US-08-422-869-1
24	46.6	4.8	994	4	US-09-023-655-1082
25	46.4	4.8	1068	4	US-09-170-496D-129
26	46.4	4.8	1068	4	US-09-170-496D-231
27	46.4	4.8	1161	1	US-08-153-848-31

28	46.4	4.8	1161	5	PCT-US93-11153-31	Sequence 31, Appl
29	46.4	4.8	2254	1	US-08-153-848-27	Sequence 27, Appl
30	46.4	4.8	2254	3	US-09-299-843A-27	Sequence 27, Appl
31	46.4	4.8	2254	4	PCT-US93-11153-27	Sequence 27, Appl
32	46.4	4.8	2254	5	PCT-US93-11153-27	Sequence 27, Appl
33	46.4	4.8	3100	4	US-09-016-434-1442	Sequence 1442, Ap
34	46.4	4.8	3119	3	US-09-299-843A-31	Sequence 31, Appl
35	46.4	4.8	3119	4	US-09-088-337B-31	Sequence 31, Appl
36	45.8	4.7	225	4	US-09-016-434-198	Sequence 198, App
37	45.8	4.7	980	4	US-09-218-467B-6	Sequence 51, Appl
38	45.8	4.7	1209	4	US-09-170-496D-51	Sequence 191, App
39	45.8	4.7	1209	4	US-09-170-496D-191	Sequence 1, Appl
40	45.8	4.7	1269	3	US-09-224-426-1	Sequence 1, Appl
41	45.8	4.7	1269	3	US-09-478-602-1	Sequence 1, Appl
42	45.8	4.7	1269	3	US-09-478-602-1	Sequence 1, Appl
43	45.8	4.7	1316	3	US-08-602-809-1	Sequence 1, Appl
44	45.8	4.7	1316	5	PCT-US95-16472-1	Sequence 1, Appl
45	45.8	4.7	1385	3	US-08-984-288-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-495-050A-164
; Sequence 164, Application US/09495050A
; Patent No. 6492505
; GENERAL INFORMATION:
; APPLICANT: Roopa, Reddy
; APPLICANT: Guegler, Karl, J.
; APPLICANT: Au-Young, Janice
; TITLE OF INVENTION: COMPOSITION FOR DETECTION OF GENES ENCODING MEMBRANE-ASSOCIATED
; FILE REFERENCE: PA-0013 US
; CURRENT APPLICATION NUMBER: US/09/495,050A
; CURRENT FILING DATE: 2000-01-31
; PRIOR FILING DATE: February 1, 1999
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: PERL Program
; SEQ ID NO 164
; LENGTH: 291
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6492505 1909132CT1
US-09-495-050A-164

Query Match 30.0%; Score 291; DB 4; Length 291;
Best Local Similarity 100.0%; Pred. No. 78-73;
Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	331	AGCATGTGAGCGGCATCAGCAGGCGCTGCTGCCATCTGTGGCCCATCTGTATC	390
Db	61	AGCATGTGAGCGGCATCAGCAGGCGCTGCTGCCATCTGTGGCCCATCTGTATC	120
Qy	391	CACGTCCGCGCCCGCCAGATACCTGTGTCATCGGTGTCCTGTCTGGGCGCTGTC	450
Db	121	CACGTCCGCGCCCGCCAGATACCTGTGTCATCGGTGTCCTGTCTGGGCGCTGTC	180
Qy	451	CTGTGCGGAGTATCTCGGAGTGGATGTTCTGTGACTTCTGTTAGTGCTGATCT	510
Db	181	CTGTGCGGAGTATCTCGGAGTGGATGTTCTGTGACTTCTGTTAGTGCTGATCT	240
Qy	511	GTGTTGGTGTGAACGTCAGATTTTCATTACATCCGTGGCTGTTTATTA	561
Db	241	GTGTTGGTGTGAACGTCAGATTTTCATTACATCCGTGGCTGTTTATTA	291

RESULT 2

US-09-016-434-330
; Sequence 330, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 330:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 275 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: CONNUT01
; CLONE: 1909132
; US-09-016-434-330

Query Match 28.4%; Score 275; DB 4; Length 275;
Best Local Similarity 100.0%; Pred. No. 2.3e-68;
Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	271	CGCCATCCCATCTCCAAATCCCTCAGTCCTGTGATGACCTTTCCTTACTTTATAGGCCTA	330
DB	1	CGCCATCCCATCTCCAAATCCCTCAGTCCTGTGATGACCTTTCCTTACTTTATAGGCCTA	60
QY	331	AGCATGTGAGCGGCATCAGACCGCGCTGCTGTCCATCTCTGTGGCCATCTGGTAC	390
DB	61	AGCATGTGAGCGGCATCAGACCGCGCTGCTGTCCATCTCTGTGGCCATCTGGTAC	120
QY	391	CACCTGCCCGCGCCCGACATACCTGTCTCATGTGTGTCTGTCTGTGGCCCTGTCC	450
DB	121	CACCTGCCCGCGCCCGACATACCTGTCTCATGTGTGTCTGTCTGTGGCCCTGTCC	180
QY	451	CTGCTGGGAGTATCCCTGGAGTGTGATGTTCTGTGACCTTCTGTGTAGTGTGTGATCT	510
DB	181	CTGCTGGGAGTATCCCTGGAGTGTGATGTTCTGTGACCTTCTGTGTAGTGTGTGATCT	240
QY	511	GTTTGGTGTGAACGTGACATTTTCATTACATGCG	545
DB	241	GTTTGGTGTGAACGTGACATTTTCATTACATGCG	275

RESULT 3

US-09-016-434-1225
; Sequence 1225, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1225:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1388 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g187388
; US-09-016-434-1225

Query Match 12.2%; Score 118.6; DB 4; Length 1388;
Best Local Similarity 49.6%; Pred. No. 9.3e-24;
Matches 415; Conservative 0; Mismatches 389; Indels 33; Gaps 3;

QY	75	GCAGACCCCTGAGCTTCACGGGGCTGACGTGATCGTTTCCCTTGTTCGGCTGACAGGAAA	134
DB	357	GCAATCCCATCGTCGACCTGGGTCAATATGAGCATCTCCCGAGTGGGTTTGTGAAA	416
QY	135	CGCGGTGTGCTCTGGCTTCCTGGGCTCGGATCGCAGGAAACGCTCTCTCCATCTACAT	194
DB	417	TGGATTCTCTCTGTGTTCTCTGCTTCGGATGAGAAGAAATCCCTTCACTGCTACAT	476
QY	195	CCTCAACTGTGTGCGCGCGACTTCCTCTTCCTTAGCGGCCACATTAATATGTTCCCGTT	254
DB	477	CACCCACCTGTCTATCGCAGACATCTCACTGCTCTTCTGTATTTTCTGTGTATGGA	536
QY	255	AGCCCTCATCAATATCCGCCATCCCATCTCCAAATCTCAGTCTGTGA-----	304
DB	537	CTATGCTTTAGATATGAGCTTTCTCTGGCCATTACTACACATTTGCACATATCACT	596
QY	305	-----TGACCTTTTCCCTACTTTTATAGCCTTAAGCATGCTGAGCGCCATPCAGACCGGCG	359
DB	597	GACCTTTTCTGTTTGGCTACAACACGGGCTCTATCTGCTGACGGCCATTAGTGGAGAG	656
QY	360	CTGCTGTCCATCTCTGTGGCCCATCTGTACCATCTGCCCGCCCGCCAGATACCTGTCTATC	419

Db 657 GTGCGTGTCACTCTTTACCCCACTGTGATCCGATGCCATGCCCCCAAGTACCAGTGGC 716
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Db 717 ATTGGTCTGCGCCCTCTGCTGCGCTCTTTCTGCTTGGTACACCAATGAGTATGTCAT 776
Qy 480 CTGTAATCTCTGTTTACTGTGCTGATTC-----TGTGTTGGTGTGAACGTGAGATTT 533
Db 777 GTGCATCAGACAGAGAAGAGAGATCACTCTCGGAATGACTGCGGAGCAGTCAATCATCTT 836
Qy 534 CATTACATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 593
Db 837 TATAGCCATCTGAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 896
Qy 594 GCTGCTGAGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 653
Db 897 GGTCTGAGATCCGGAAGACACAGTGGCTTCCCATTCCTCCCAAGCTTTACATAGTCAT 956
Qy 654 CTTCTCAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 713
Db 957 CATGCTCAGATCAATATATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1006
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Db 1007 --TTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1064
Qy 774 TTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 833
Db 1065 GCTCTCTTCCCAATCAACAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1124
Qy 834 TAGGAGCGTCAAAATAGGAGAGTCAAGTGTGCTTCCAGAGGGCTCTGCAAGG 890
Db 1125 TAAGAAGAGAGATTCAGGAGTCTTAAAGTGTCTGACGAGGGCTTTCAAGA 1181

RESULT 4

PCT-US93-06251-26
; Sequence 26, Application PC/TUS9306251
; GENERAL INFORMATION:
; APPLICANT: Wickstrom, Eric and Rife, Jason P.
; TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing
; TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: NY
; COUNTRY: USA
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/06251
; FILING DATE: 19930630
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Digilio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 8586
; TELEPHONE: 516-742-4343
; TELEFAX: 516-742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1388 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double

; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US93-06251-26
Query Match 12.2%; Score 118.6; DB 5; Length 1388;
Best Local Similarity 49.6%; Pred. No. 9.3e-24;
Matches 415; Conservative 0; Mismatches 389; Indels 33; Gaps 3;
Qy 75 GCAGACCCCTGAGTTTACCGGGCTGACGTGCAATCGTTTCCCTTGTGCGCTGACAGGAA 134
Db 357 GCAATCCCATCGTGCATCGGTGCTATTATGAGCATCTCCAGTGGGTTTGTGAGAA 416
Qy 135 CGGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 194
Db 417 TGGATTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 476
Qy 195 CTTCAACCTGGTGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 254
Db 477 CACCCACCTGCTATCGCAGACATCTCACTGCTCTTCTGTAATTTTCTGCTGCTATCGA 536
Qy 255 ACSCCTCAATATCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 304
Db 537 CTATGCTTTAGATATGAGCTTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 596
Qy 305 -----TGACCTTTCCCTACTTTATAGGCTTAAGCATGCTGAGCGCCATCAGACCCAGCG 359
Db 597 GACTTTTCTGTTGGCTTACAACACAGGGCTCTATCTGCTGAGGGCCATTAGTGTGGAGAG 656
Qy 360 CTGCT 419
Db 657 GTGCT 716
Qy 420 GGTCAATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 479
Db 717 ATGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 776
Qy 480 CTGTAATCTCTCTTTAGTGGTGTCTGATTC-----TGTGTTGGTGTGAACGTGAGATTT 533
Db 777 GTGCATCGACAGAGAAGAGAGTCACTCTCGGAATGACTGCGGAGCAGTCAATCATCTT 836
Qy 534 CATTACATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 593
Db 837 TATAGCATCTGAGCTTCTGCTGCTTTCAGGCCCTCATGCTGCTGCTGCTGCTGCTGCTGCT 896
Qy 594 GCTGGTCAAGATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 653
Db 897 GGTCTGAGATCCGGAAGACACAGTGGCTTCCCATTCCTCCAGCTTTACATAGTCAT 956
Qy 654 CTTCTCAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 713
Db 957 CATGCTCAGATCAATATATCT 1006
Qy 714 GTTTTCCAGGATCCACCTGAGTGGAAAGTCTTATTTTGTGCTGCTGCTGCTGCTGCTGCTGCT 773
Db 1007 --TTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1064
Qy 774 TTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 833
Db 1065 GCTCTTCTCCCAATCAACAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1124
Qy 834 TAGGAGCGTCAAAATAGGAGAGTCAAGTGTGCTTCCAGAGGGCTCTGCAAGG 890
Db 1125 TAAGAAGAGAGATTCAGGAGTCTTAAAGTGTCTGACGAGGGCTTTCAAGA 1181

RESULT 5

US-09-484-970B-134
; Sequence 134, Application US/09484970B
; Patent No. 6426186
; GENERAL INFORMATION:
; APPLICANT: Jones, Karen A.
; APPLICANT: Volkman, Wayne
; APPLICANT: Walker, Michael G.

QY 275 ATCCCATCTCCAAAATCCTCAGTCTGATGACCTTTCCCTACTTTATAGCCCTAAGCA 334
DB 1424 TTTTATCCCTGATTTCTTGCCATATTGTCTCCCTTCTCTTTGAGGTGTCTCTGTC 1483
QY 335 TGCTGAGCGCCATCAGCACGAGCGCTCCCTGTCATCCCTGTGCGCCATCTGGTACCACT 394
DB 1484 TCCTGGTGGCCATCAGCACGAGCGGTGTGTGTCTCTCTCTCCCATCTGGTACAGAT 1543
QY 395 GCCGCGCCCGAGATACCTGTGTCATCGGTGTCATGTCCTCTCTGGGCCCTGTCCTGTC 454
DB 1544 GCCACCGCCGAAAATACACATCTAATGTTGTCGTGACCCCTCATCTGGGGCTGCTTTT 1603
QY 455 TGCGAGATCTCTGGAGTGGATGTTCTGTGACTTCTCTGTTAGTGTGCTGATTTCTGTT 514
DB 1604 GCATCAACATAGTAAATACATTTTCTTAACTTACTGGAACATGTAAAGGCATGTGTCA 1663
QY 515 GGTGTGAACGTGACATTTATTACAATCGGTGGTCTGTTTATATGTTGTTCTCT 574
DB 1664 TATTTCTAAAG-----CTTCTGGGCTCTTCCATGCTATCTTCACTTGTGATGT 1714
QY 575 GTGGTCCAGCCTGCTGCTGTGTCAGGATTTCTGTGATCCCGAAGATGCGGTGA 634
DB 1715 GTGTGTCAGTCTGACTCTACTCAATTAGATTCCTGTGCTGCTCCAGCAGCAAAAGGCCA 1774
QY 635 CCAGCTGTAGTGACCATCTCTCCACAGTGTGCTTCTCTCTGTCGTGGCTGCT 694
DB 1775 CCAGGCTGTATGCGGTGTGAGATCTCGGCCCATGTTCTACTCTGGGCCCTACCCC 1834
QY 695 TTGGCATTCAGTGGGCCCTGTTTCCAGGATCCACTGATGGAAGTCTTATTTGTC 754
DB 1835 TGAGC-----GTGGCACCCCTCATACAGATTCGAATGTTGTACCA 1879
QY 755 ATGTGCACTAGTTTCATTTTCTGTGCTGCTTTAAAGAGTGTGCAAGTCCAACTTATTT 814
DB 1880 CCTCTATTATTTCTTGTTCCT---CATTTAAACAGCAGCGCCCAACCTATCATTT 1936
QY 815 ACTTCTCTGCTGCTCTTTAGCAGCGTCAAAATAGCAGAACTGAGTGTGTTCTCC 874
DB 1937 ATTCTTCTGGGGAGCTCAAGAAAGAGCTGAGAACTCTCAGATGATTTCTCC 1996
QY 875 AGAGGCTCTGAGGACACGCTGAGGTGG 904
DB 1997 AACGGCGTTAGCAGATAGCCAGAGGTGG 2026

RESULT 7

5320941-1
; Patent No. 5320941
; APPLICANT: Young, Dallen; Wigler, Michael H.; Fasano
; Ottavio
; TITLE OF INVENTION: DNA SEQUENCES ENCODING MAS ONHCOGENE,
; POLYPEPTIDES ENCODED THEREFROM AND DIAGNOSTIC AND OTHER METHODS
; BASED THEREFROM
; NUMBER OF SEQUENCES: 2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/06/872,087
; FILING DATE: 06-JUN-1986
; SEQ ID NO: 1:
; LENGTH: 1327
5320941-1

Query Match 9.7%; Score 94.2; DB 6; Length 1327;
Best Local Similarity 48.5%; Pred. No. 7.3e-17;
Matches 338; Conservative 0; Mismatches 338; Indels 21; Gaps 2;

QY 75 GCAGACCTCTGAGCTTACGCGGCTGACGTGCATCGTTTCCCTTGTGCGCTGACAGGAAA 134
DB 356 GCAATCCCATCTGTCATCTGGTCAATATTAGACATCTCCCAAGTGGGTTTGTGAGAA 415
QY 135 CGCGGTGTGCTGTGCTCTGTGGCTGCGGCATGCGCAGGAAAGCTGTCTCATCATCAT 194
DB 416 TGGGATTTCTCTGTGTTCTGTGCTTCCGGATGAGAGAAATCCCTTCACTGTCTACAT 475

QY 195 CTTCAACCTGTGCGCGGAGCTTCTCTTCTTAGCGGCCACATATATGTTGCGCGTT 254
DB 476 CACCCACCTGTCTATCGCAGACATCTCACTCTCTTCTGTAATTTTCACTCTGTCTATCGA 535
QY 255 AGCCCTCATCATATCCGCCATCCCATCTCCAAAATCTCAGTCTCTGTGA----- 304
DB 536 CTATGCTTTAGATTTAGAGCTTTCTTCTGGCCATTACTACAAATTTGTACAAATTAATCAGT 595
QY 305 -----TGACCTTTCCCTACTTTTATAGCCCTAAGCATGCTGAGCGCCATCAGCACCCAGCG 359
DB 596 GAGTTTCTGTTTGGCTACAAACAGGCGCTCTATCTGCTGACGGCCATTAGTGTGGAGAG 655
QY 360 CTGCTGTCCATCTCTGCGCCATCTGGTACCATCTGCGCCCGCCCGCCAGATACCTGTGATC 419
DB 656 GTGCTGTGAGTCTCTTTTACCCCATCTGTTGACCATGCGCATCGCCCAAGTACCAAGTCGCG 715
QY 420 GGTATGTTGTCCTCTCTGCGCCCTGCTCCCTGCTGCGGAGTATCTCTGAGTGGATGTT 479
DB 716 ATTGGTCTGTGCGCTTCTGTGGCTCTTCTGCTGCTGTTGTTGACCATGAGTATGTCAT 775
QY 480 CTGTGATTC-----CTGTTTAGTGTGCTGATTTCTGTTTGTGTGAAACGTGATTT 533
DB 776 GTGATCCACACAGAAAGAGAGTGAATCTCCGAATGACTGCCACAGCTCATCATCTT 835
QY 534 CATTACAATCGGTGCTGCTGTTTATGTTGTTGTTCTCTGTTGCTGCGCTGAGCTGCT 593
DB 836 TATAGCATCTCTGAGCTTCTGCTGCTTCTGAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCT 895
QY 594 GCTGGTCAAGATTTCTCTGTGATCCCGAAGATGCGCTGACAGGCTGTGATGACCAT 653
DB 896 GGTGCTGAAGATCCCGAAGAACAGTGGCTTCCCATTTCTCCAAAGCTTTACATAGTCAT 955
QY 654 CTCTCTCAGAGTCTGCTCTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 713
DB 956 CATGGTCACCATCATTTATCTCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1015
QY 714 GTTTTCCAGGATCCACTGATTTGAAAGTCTTATTT 750
DB 1016 GTACTACAGTAGCGCAACCCCTTCTTACTTCTTT 1052

RESULT 8

US-09-016-434-210
; Sequence 210, Application US/09016434
; Patent No. 650938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:


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;
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: MSHIM4.001APC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 714-760-0404
; TELEFAX: 714-760-9502
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2911 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; US-08-981-825-5

Query Match 6.1%; Score 59.2; DB 3; Length 2911;
Best Local Similarity 48.8%; Pred. No. 8.6e-07;
Matches 200; Conservative 0; Mismatches 198; Indels 12; Gaps 1;

Qy 96 GGTGACGTCATCGTTTCCCTTGTGCGCTGACAGAAACGCGGTGTGCTCTGGCTCCT 155
Db |||||
Qy 156 GGGCTGCCGATCGCAGAACGCTGCTCCATCTACATCTCAACCTGTCGCGCCGA 215
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Qy 283 GGGCTGCCGATCGCAGAACGCTGCTCCATCTACATCTCAACCTGTCGCGCCGA 342
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Qy 216 CTTCTCT-----CTTCTTAGCGGCCACATATATGTTTCGCCGTTACGCTCAT 263
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Qy 264 CAATATCGCCATCCCATCTCCAAATCTCAGTCTGTGATGACCTTCCCTACTTTAT 323
Db |||||
Qy 403 GGAGCTGGGCACACCTTCTGCAAACTGACCTCTCCATCTTCTTCTCAACATGTTCCG 462
Db |||||
Qy 324 AGGCCTAAGCATGCTGAGCGCCATCAGACCGAGCGTGCCTGTCCATCCTGTGGCCCAT 383
Db |||||
Qy 463 CAGCGGCTTCTGCTCAGCGCCATCAGCTGAGCGCTGCTGCTGAGTGTGCTGGCCGGT 522
Db |||||
Qy 384 CTGTGTACACTGCGCGCCGCCAGATACCTGTCTCATCGGTCAATGTTCTGCTCTGGGC 443
Db |||||
Qy 523 GTGGGCGCAGAACCCGACCCGCTGCGCGCGCCGCAAAAGTCTGCTGTGTTTGGGC 582
Db |||||
Qy 444 CTTGTCCTCTGCTGCGGAGTATCTTGAGTGATGATGTTCTGTGATCTTCTGT 493
Db |||||
Qy 583 ACTAGCGGTGCTCAACACGGTGCCTATTTCTGTTCCGGGACACCATCT 632
Db |||||

RESULT 11
US-09-480-784-5
; Sequence 5, Application US/09480784
; Patent No. 6156186
; GENERAL INFORMATION:
; APPLICANT: OGAWA, KAZUYAUKI
; TANAKA, KAZUYA
; NAGATA, KINYA
; TAKANO, SYOICHI
; TITLE OF INVENTION: Th2, GENE (B19) ENCODING THE SAME, AND
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible

;
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/480,784
; FILING DATE: 10-Jan-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/981,825
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: MSHIM4.001APC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 714-760-0404
; TELEFAX: 714-760-9502
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2911 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-480-784-5

Query Match 6.1%; Score 59.2; DB 3; Length 2911;
Best Local Similarity 48.8%; Pred. No. 8.6e-07;
Matches 200; Conservative 0; Mismatches 198; Indels 12; Gaps 1;

Qy 96 GGTGACGTCATCGTTTCCCTTGTGCGCTGACAGAAACGCGGTGTGCTCTGGCTCCT 155
Db |||||
Qy 156 GGGCTGCCGATCGCAGAACGCTGCTCCATCTACATCTCAACCTGTCGCGCCGA 215
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Qy 283 GGGCTGCCGATCGCAGAACGCTGCTCCATCTACATCTCAACCTGTCGCGCCGA 342
Db |||||
Qy 216 CTTCTCT-----CTTCTTAGCGGCCACATATATGTTTCGCCGTTACGCTCAT 263
Db |||||
Qy 264 CAATATCGCCATCCCATCTCCAAATCTCAGTCTGTGATGACCTTCCCTACTTTAT 323
Db |||||
Qy 403 GGAGCTGGGCACACCTTCTGCAAACTGACCTCTCCATCTTCTTCTCAACATGTTCCG 462
Db |||||
Qy 324 AGGCCTAAGCATGCTGAGCGCCATCAGACCGAGCGTGCCTGTCCATCCTGTGGCCCAT 383
Db |||||
Qy 463 CAGCGGCTTCTGCTCAGCGCCATCAGCTGAGCGCTGCTGCTGAGTGTGCTGGCCGGT 522
Db |||||
Qy 384 CTGTGTACACTGCGCGCCGCCAGATACCTGTCTCATCGGTCAATGTTCTGCTCTGGGC 443
Db |||||
Qy 523 GTGGGCGCAGAACCCGACCCGCTGCGCGCGCCGCAAAAGTCTGCTGTGTTTGGGC 582
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Qy 444 CTTGTCCTCTGCTGCGGAGTATCTTGAGTGATGATGTTCTGTGATCTTCTGT 493
Db |||||
Qy 583 ACTAGCGGTGCTCAACACGGTGCCTATTTCTGTTCCGGGACACCATCT 632
Db |||||

RESULT 12
US-09-016-434-1188
; Sequence 1188, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Sellhammer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 FORSTER DRIVE
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..264
US-08-513-974B-337

Query Match      5.3%; Score 51.6; DB 3; Length 265;
Best Local Similarity 56.5%; Pred. No. 3.7e-05;
Matches 96; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

QY      118  GTGCGCTGACAGGAAACGCGTTGTGCTCTGGCTCCTGGGCTGCCGATCGGAGGAC 177
Db      1  GTGGGCATGGTGGGCAACGTGCTGCTCTGGTTCTTCGGTTCTCCATCAAGAGGACC 60

QY      178  GCTGTCTCCATCTACATCTCAACCTGGTCCGGCGGACTTCCTCTTCTTAGGGCCAC 237
Db      61  CCTTCTCCGTCTACTTCTGACCTGGCCAGCGCGGCGCTACTCTTCAGCAAG 120

QY      238  ATTATATGTTCCCGTTACGCTCATCAATATCCGCCATCCCATCTCCAA 287
Db      121  GCCGTGTTCTCCCTGCTGAACGCCGGCGGCTTCCTGGGCACCTTCGCCCA 170
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Search completed: July 4, 2004, 07:23:24
Job time : 97 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 4, 2004, 06:30:08 ; Search time 525 Seconds
(without alignments)
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Title: US-09-787-879C-3

Perfect score: 969

Sequence: 1 atggattcaaccatccagct.....gaagcagatggagcagtga 969

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 3163042 seqs, 2412103800 residues

Total number of hits satisfying chosen parameters: 6326084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.*

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- 3: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
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- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
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- 17: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
- 18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
- 19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	969	100.0	969	9	US-09-995-225-19
2	969	100.0	969	10	US-09-995-225-19
3	969	100.0	1400	15	US-10-183-116-30
4	969	100.0	1400	15	US-10-225-567A-673
5	969	100.0	2618	12	US-09-867-570-1
6	969	100.0	8622	12	US-09-867-570-3
7	965.8	99.7	969	13	US-10-401-397A-1
8	965.8	99.7	1369	16	US-10-292-798-1273
9	964.2	99.5	969	13	US-10-391-074-1
10	845.8	87.3	909	15	US-10-237-467-9
11	833	86.0	969	9	US-09-995-225-17
12	833	86.0	969	10	US-09-995-225-17
13	833	86.0	969	15	US-10-237-467-3
14	833	86.0	1369	16	US-10-292-798-1041

15	833	86.0	1604	15	US-10-183-116-32	Sequence 32, Appl
16	833	86.0	1604	15	US-10-225-567A-688	Sequence 688, App
17	829.8	85.6	969	13	US-10-343-650A-43	Sequence 43, Appl
18	829.8	85.6	969	15	US-10-079-384-3	Sequence 3, Appl
19	829.8	85.6	969	15	US-10-240-998-3	Sequence 3, Appl
20	829.8	85.6	969	15	US-10-321-807-19	Sequence 19, Appl
21	829.8	85.6	969	15	US-10-237-467-11	Sequence 11, Appl
22	829.8	85.6	969	13	US-10-072-012-171	Sequence 171, App
23	829.8	85.6	1369	15	US-10-017-161-1055	Sequence 1055, App
24	829.8	85.6	1369	16	US-10-292-798-897	Sequence 897, App
25	829.8	85.6	2040	15	US-10-183-116-15	Sequence 15, Appl
26	826.2	85.3	1370	15	US-10-017-161-1599	Sequence 1599, App
27	821.2	84.7	964	13	US-10-072-012-173	Sequence 173, App
28	794.4	82.0	1005	13	US-10-072-012-177	Sequence 177, App
29	792.2	81.8	966	15	US-10-240-998-9	Sequence 9, Appl
30	769.6	79.4	966	15	US-10-240-998-6	Sequence 6, Appl
31	764.2	78.9	994	13	US-10-072-012-169	Sequence 169, App
32	729.4	75.3	1987	15	US-10-219-834-7	Sequence 7, Appl
33	697.4	72.0	769	15	US-10-101-510-239	Sequence 239, App
34	618.8	63.9	961	15	US-10-240-998-7	Sequence 7, Appl
35	596.6	61.6	1003	10	US-09-800-321A-30	Sequence 30, Appl
36	596.6	61.6	1030	13	US-10-072-012-175	Sequence 175, App
37	587.2	60.6	994	15	US-10-240-998-8	Sequence 8, Appl
38	587.2	60.6	1163	9	US-09-750-373-11	Sequence 11, Appl
39	587.2	60.6	1300	15	US-10-183-116-17	Sequence 17, Appl
40	587.2	60.6	1300	15	US-10-225-567A-648	Sequence 648, App
41	587.2	60.6	1393	15	US-10-017-161-1053	Sequence 1053, App
42	587.2	60.6	1393	16	US-10-292-798-895	Sequence 895, App
43	587.2	60.6	1394	16	US-10-292-798-1269	Sequence 1269, App
44	587.2	60.6	1770	9	US-09-920-068A-8	Sequence 8, Appl
45	585.8	60.5	993	9	US-09-826-508-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1

US-09-995-225-19
; Sequence 19, Application US/0995225
; Publication No. US20020193584A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Chu, Zhi Liang
; APPLICANT: Dang, Huong T.
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Pride, Cameron
; TITLE OF INVENTION: Endogenous And No. US20020193584A1-Endogenous Versions of Human
; FILE OF INVENTION: Receivers
; FILE REFERENCE: AREN-0308
; CURRENT APPLICATION NUMBER: US/09/995,225
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: PCT/US99/23938
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/253,404
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/255,366
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/270,286
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/282,365
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/270,266
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/282,032
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,358
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,356
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/290,917
; PRIOR FILING DATE: 2001-05-14

;; PRIOR APPLICATION NUMBER: 60/309,208
;; PRIOR FILING DATE: 2001-07-31
;; NUMBER OF SEQ ID NOS: 67
;; SOFTWARE: Patent in version 3.1
;; SEQ ID NO 19
;; LENGTH: 969
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: No. US20020193584A1el Sequence
US-09-995-225-19

Query Match 100.0%; Score 969; DB 9; Length 969;
Best Local Similarity 100.0%; Pred. No. 1.2e-291;
Matches 969; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGATTCAACCATCCAGTCTTGGGTACAGAACTGACACCAATCAACGGAGCTGAGGAG 60
Db 1 ATGGATTCAACCATCCAGTCTTGGGTACAGAACTGACACCAATCAACGGAGCTGAGGAG 60

QY 61 ATCTCTTGTCTACAGAGACCCCTGAGCTTACGGGGCTGACGTGATCGTTCCCTTGTG 120
Db 61 ATCTCTTGTCTACAGAGACCCCTGAGCTTACGGGGCTGACGTGATCGTTCCCTTGTG 120

QY 121 GCGCTGACAGAAACCGGTGTGCTCTGGCTCTGGGCTGCGGATGCGGAGGACGCT 180
Db 121 GCGCTGACAGAAACCGGTGTGCTCTGGCTCTGGGCTGCGGATGCGGAGGACGCT 180

QY 181 GTCTCCATCTACATCCTCAACCTGTGTGCGGCGGACTTCTCTTCTTACGCGCCACATT 240
Db 181 GTCTCCATCTACATCCTCAACCTGTGTGCGGCGGACTTCTCTTCTTACGCGCCACATT 240

QY 241 ATATGTCGCGGTAGCGCTCATCAATATCCGCCATCCCATCTCCAAATCTCTAGTCT 300
Db 241 ATATGTCGCGGTAGCGCTCATCAATATCCGCCATCCCATCTCCAAATCTCTAGTCT 300

QY 301 GTGATGACCTTCCCTACTTTATAGGCTTAAGCATCTGAGCGCCATCAGCACCGAGCG 360
Db 301 GTGATGACCTTCCCTACTTTATAGGCTTAAGCATCTGAGCGCCATCAGCACCGAGCG 360

QY 361 TGCGTGTCACTCTGGGCCATCTGGTACCATCTGGCGGCGCCGAGATACCTGTCTATCG 420
Db 361 TGCGTGTCACTCTGGGCCATCTGGTACCATCTGGCGGCGCCGAGATACCTGTCTATCG 420

QY 421 GTCATGTGTCTCTGCTCTGGGCCCTCTCCCTCTGCGGAGTATCTCTGAGTGGATGTT 480
Db 421 GTCATGTGTCTCTGCTCTGGGCCCTCTCCCTCTGCGGAGTATCTCTGAGTGGATGTT 480

QY 481 TGTGACTTCTGTTAGTGTGTGATCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 540
Db 481 TGTGACTTCTGTTAGTGTGTGATCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 540

QY 541 ATCCGCTGGCTGTTTCTTCTGTTGTTCTCTGTTGTTCTGTTGTTCTGTTGTTCTGTT 600
Db 541 ATCCGCTGGCTGTTTCTTCTGTTGTTCTCTGTTGTTCTGTTGTTCTGTTGTTCTGTT 600

QY 601 AGGATCTCTGTGATCCCGAAGATCCCGTGTGATCCCGTGTGATCCCGTGTGATCCCGT 660
Db 601 AGGATCTCTGTGATCCCGAAGATCCCGTGTGATCCCGTGTGATCCCGTGTGATCCCGT 660

QY 661 ACAGTGTGCTTCTCTCTCTGTTGTTCTGTTGTTCTGTTGTTCTGTTGTTCTGTTGTT 720
Db 661 ACAGTGTGCTTCTCTCTCTGTTGTTCTGTTGTTCTGTTGTTCTGTTGTTCTGTTGTT 720

QY 721 AGGATCCACCTGGATTGAAAGTCTTATTTGTCTATGTCATGTCATGTCATGTCATGTC 780
Db 721 AGGATCCACCTGGATTGAAAGTCTTATTTGTCTATGTCATGTCATGTCATGTCATGTC 780

QY 781 TCCGCTCTTACAGAGTCCCAAGCCCATCAATTTACTTCTTCTGTTGTTCTTCTTCTTCT 840
Db 781 TCCGCTCTTACAGAGTCCCAAGCCCATCAATTTACTTCTTCTGTTGTTCTTCTTCTTCT 840

QY 841 CGTCAAAATAGGACAGACCTGAAGCTGTGTTCTCCAGAGGGCTCTGACGACACGCTGTAG 900

Db 841 CGTCAAAATAGGACAGACCTGAAGCTGTGTTCTCCAGAGGGCTCTGACGACGCTGAG 900

QY 901 GTGGATGAAGTGGAGGGTCTTCTCAGGAAACCTCTGAGCTGTGCGGAAACGAGATTG 960

Db 901 GTGGATGAAGTGGAGGGTCTTCTCAGGAAACCTCTGAGCTGTGCGGAAACGAGATTG 960

QY 961 GAGCAGTGA 969

Db 961 GAGCAGTGA 969

RESULT 2
US-09-995-225-19
; Sequence 19, Application US/09995225
; Publication No. US20030139588A9
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Chu, Zhi Liang
; APPLICANT: Dang, Huong T.
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Pride, Cameron
; TITLE OF INVENTION: Endogenous And No. US20030139588A9-Endogenous Versions of Human
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0308
; CURRENT APPLICATION NUMBER: US/09/995,225
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 03/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: PCT/US99/23938
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/253,404
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/255,366
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/270,286
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/282,365
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/270,266
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/282,032
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,358
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,356
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/290,917
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/309,208
; PRIOR FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 19
; LENGTH: 969
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. US20030139588A9el Sequence
US-09-995-225-19

Query Match 100.0%; Score 969; DB 10; Length 969;
Best Local Similarity 100.0%; Pred. No. 1.2e-291;
Matches 969; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGATTCAACCATCCAGTCTTGGGTACAGAACTGACACCAATCAACGGAGCTGAGGAG 60
Db 1 ATGGATTCAACCATCCAGTCTTGGGTACAGAACTGACACCAATCAACGGAGCTGAGGAG 60

QY 61 ACTCTCTGTCTACAGAGACCCCTGAGCTTACGGGGCTGAGCTGATCGTTCCCTTGTG 120
Db 61 ACTCTCTGTCTACAGAGACCCCTGAGCTTACGGGGCTGAGCTGATCGTTCCCTTGTG 120

121 GCGTGCAGGAAACGGGTTGTCTCTGGCTCCTGGCTCGCGATGCGCAGGAAACGCT 180
Db GCGCTGACGAAACGGGTTGTCTCTGGCTCCTGGCTCGCGATGCGCAGGAAACGCT 180
181 GTCTCCATCTACATCCTCAACCTGCTCGGCGCGACTTCTCTCTCTAGGGGCAACATT 240
Db GTCTCCATCTACATCCTCAACCTGCTCGGCGCGACTTCTCTCTCTAGGGGCAACATT 240
241 ATATGTTCCGCGTTACGGCTCATCAATATCGCCATCCCATCTCCAAATCCTCAGTCCT 300
Db ATATGTTCCGCGTTACGGCTCATCAATATCGCCATCCCATCTCCAAATCCTCAGTCCT 300
301 GTGATGACCTTTCCCTACTTTATAGGCTTAAGCATGCTGAGCGCATCAGACCGAGCGC 360
Db GTGATGACCTTTCCCTACTTTATAGGCTTAAGCATGCTGAGCGCATCAGACCGAGCGC 360
361 TGCCTGTCATCTCTGCGCCCATCTGTTACCATGCGCGCGCCGAGATCCTGTCATCG 420
Db TGCCTGTCATCTCTGCGCCCATCTGTTACCATGCGCGCGCCGAGATCCTGTCATCG 420
421 GTCATGTGTCTCTCTGCGCCCATCTGTTACCATGCGCGCGCCGAGATCCTGTCATCG 480
Db GTCATGTGTCTCTCTGCGCCCATCTGTTACCATGCGCGCGCCGAGATCCTGTCATCG 480
481 TGTGATCTCTCTTTAGTGGTCTGATCTGTTGGTGTGAACCTCAGATTTCAATACA 540
Db TGTGATCTCTCTTTAGTGGTCTGATCTGTTGGTGTGAACCTCAGATTTCAATACA 540
541 ATCGCGTGGCTGGTCTTTTATGTTGTGTTCTCTGTTGGTGTGAGCTGCTGCTGCTC 600
Db ATCGCGTGGCTGGTCTTTTATGTTGTGTTCTCTGTTGGTGTGAGCTGCTGCTGCTC 600
601 AGGATTTCTGTGGATCCCGGAAGATGCGGTGACAGCGCTGATGACCATCTCTCCTC 660
Db AGGATTTCTGTGGATCCCGGAAGATGCGGTGACAGCGCTGATGACCATCTCTCCTC 660
661 ACAGTGTCTGCTCTCTCTCTCTGTTGGTCTGTTGGTCTGTTGGTCTGTTGGTCTG 720
Db ACAGTGTCTGCTCTCTCTCTCTGTTGGTCTGTTGGTCTGTTGGTCTGTTGGTCTG 720
721 AGGATCCACTGGATGGAAGCTTTATTTTGTGATGTCATCTAGTTTCAATTTCTG 780
Db AGGATCCACTGGATGGAAGCTTTATTTTGTGATGTCATCTAGTTTCAATTTCTG 780
781 TCGCTCTTAACAGAGTGCACCCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 840
Db TCGCTCTTAACAGAGTGCACCCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 840
841 CGTCAAAATAGGAGAACCTGAAGCTGTTCTCCAGAGGCTCTCCAGGACACGCTGAG 900
Db CGTCAAAATAGGAGAACCTGAAGCTGTTCTCCAGAGGCTCTCCAGGACACGCTGAG 900
901 GTGGATGAGGTGAGGGTGGCTTCTCTAGGAAACCTGAGCTGTGCGGAGCAGATTG 960
Db GTGGATGAGGTGAGGGTGGCTTCTCTAGGAAACCTGAGCTGTGCGGAGCAGATTG 960
961 GAGCAGTGA 969
Db GAGCAGTGA 969

RESULT 3
US-10-183-116-30
; Sequence 30, Application US/10183116
; Publication No. US20030092035A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David J.
; APPLICANT: Dong, Xinzhang
; APPLICANT: Zylka, Mark
; APPLICANT: Simon, Melvin
; APPLICANT: Han, Sang-kyou
; TITLE OF INVENTION: PAIN SIGNALING MOLECULES
; FILE REFERENCE: CALTE.4CLCP1

CURRENT APPLICATION NUMBER: US/10/183,116
CURRENT FILING DATE: 2002-06-26
PRIOR APPLICATION NUMBER: US 60/222,344
PRIOR FILING DATE: 2000-08-01
PRIOR APPLICATION NUMBER: US 60/202,027
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 09/704,707
PRIOR FILING DATE: 2000-11-03
PRIOR APPLICATION NUMBER: US 60/285,493
PRIOR FILING DATE: 2001-04-19
PRIOR APPLICATION NUMBER: US 09/849,869
PRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 109
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 30
LENGTH: 1400
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (332)...(1297)
US-10-183-116-30
Query Match 100.0%; Score 969; DB 15; Length 1400;
Best Local Similarity 100.0%; Pred. No. 1.5e-291;
Matches 969; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGATTTAAACCATCCCGAGTCTTGGGTACAGAACTGACACCAATCAACGACGCTGAGGAG 60
Db 332 ATGATTTAAACCATCCCGAGTCTTGGGTACAGAACTGACACCAATCAACGACGCTGAGGAG 391
QY 61 ACTCTTTGTCTACAGCAGACCTTGAGCTTCAACGGGCTGACGTGCTATCGTTTCCCTTGTG 120
Db 392 ACTCTTTGTCTACAGCAGACCTTGAGCTTCAACGGGCTGACGTGCTATCGTTTCCCTTGTG 451
QY 121 GCGTGCAGAGAAACCGGTTGTCTGTGCTCCTGGGCTGCGGCTGCGGCTGCGGCAAGCGCT 180
Db 452 GCGTGCAGAGAAACCGGTTGTCTGTGCTCCTGGGCTGCGGCTGCGGCTGCGGCAAGCGCT 511
QY 181 GTCTCCATCTACATCTCTCAACCTGTTGGTCTGCGGCGGCTTCTCTCTTACGGGCAACATT 240
Db 512 GTCTCCATCTACATCTCTCAACCTGTTGGTCTGCGGCGGCTTCTCTCTTACGGGCAACATT 571
QY 241 ATATGTTTGGCGGTTAGCGCTCATCAATATCCGCCATCCCATCTCCAAATCTCAGTCCT 300
Db 572 ATATGTTTGGCGGTTAGCGCTCATCAATATCCGCCATCCCATCTCCAAATCTCAGTCCT 631
QY 301 GTGATGACCTTTCCCTACTTTTATAGGCTTAAGCATGCTGAGCGCCATCAGACCGAGCGC 360
Db 632 GTGATGACCTTTCCCTACTTTTATAGGCTTAAGCATGCTGAGCGCCATCAGACCGAGCGC 691
QY 361 TGCCTGTCCATCTCTGTGGCCCATCTGTTACCACTGCGCGCGCCGCGCCAGATACCTGTATCG 420
Db 692 TGCCTGTCCATCTCTGTGGCCCATCTGTTACCACTGCGCGCGCCGCGCCAGATACCTGTATCG 751
QY 421 GTCATGTGTCTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
Db 752 GTCATGTGTCTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 811
QY 481 TGTGACTTCTGTTTGTGTTGTGTTGTGTTGTGTTGTGTTGTGTTGTGTTGTGTTGTGTTGT 540
Db 812 TGTGACTTCTGTTTGTGTTGTGTTGTGTTGTGTTGTGTTGTGTTGTGTTGTGTTGTGTTGT 871
QY 541 ATCGCGTGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 600
Db 872 ATCGCGTGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 931
QY 601 AGGATTTCTGTGATCCCGGAAGATGCGGTGACAGGCTGTACGTGACGATCCTCCTCCTC 660
Db 932 AGGATTTCTGTGATCCCGGAAGATGCGGTGACAGGCTGTACGTGACGATCCTCCTCCTC 991
QY 661 ACAGTGTGTGTTTCTCTCTCTGTTGGCTGCTGTTGGCTGCTGTTGGCTGCTGTTGGCTGCT 720
Db 991 ACAGTGTGTGTTTCTCTCTCTGTTGGCTGCTGTTGGCTGCTGTTGGCTGCTGTTGGCTGCT 720

Db 492 ATGGATTCAACCAATCCAGAGTCTTGGGTACAGAACTGACCAATCAACGAGCTGAGGAG 551
Qy 61 ACTCTTGTCTAACAGCAGACCTGAGCTTACGCGGCTGACGTGCATCTGTTCCCTTGTTC 120
Db 552 ACTCTTGTCTAACAGCAGACCTGAGCTTACGCGGCTGACGTGCATCTGTTCCCTTGTTC 611
Qy 121 GCGGTGACAGAAACCGGGTGTGCTCTGGCTCTGGCTGCGGCTGCGCATCGCAGAACGCT 180
Db 612 GCGGTGACAGAAACCGGGTGTGCTCTGGCTCTGGCTGCGGCTGCGCATCGCAGAACGCT 671
Qy 181 GTCTCCATCTACATCTCTCAACTGGTGGCGGCCGACTTCTCTCTCTCTCTCTCTCTCTCT 240
Db 672 GTCTCCATCTACATCTCTCAACTGGTGGCGGCCGACTTCTCTCTCTCTCTCTCTCTCTCT 731
Qy 241 ATATGTTGCGCGTTACGCTCATCAATATCCGCCATCCCATCTCCAAATCTCTAGTCT 300
Db 732 ATATGTTGCGCGTTACGCTCATCAATATCCGCCATCCCATCTCCAAATCTCTAGTCT 791
Qy 301 GTGATGACCTTCT 360
Db 792 GTGATGACCTTCT 851
Qy 361 TGCCTGTCCATCT 420
Db 852 TGCCTGTCCATCT 911
Qy 421 GTCATGTGTCT 480
Db 912 GTCATGTGTCT 971
Qy 481 TGTGACTTCT 540
Db 972 TGTGACTTCT 1031
Qy 541 ATCGGTGGCTGGTCT 600
Db 1032 ATCGGTGGCTGGTCT 1091
Qy 601 AGGATTCCTCTGGAATCCCGAAGATGCGGTGACCAAGCTGTGACCATCTCTCTCTCTCT 660
Db 1092 AGGATTCCTCTGGAATCCCGAAGATGCGGTGACCAAGCTGTGACCATCTCTCTCTCTCT 1151
Qy 661 ACAGTGTCT 720
Db 1152 ACAGTGTCT 1211
Qy 721 AGGATCCACCTGGATTGGAAGTCTTATTTTGTATGTGCAATCTAGATTCTCTCTCTCTCT 780
Db 1212 AGGATCCACCTGGATTGGAAGTCTTATTTTGTATGTGCAATCTAGATTCTCTCTCTCTCT 1271
Qy 781 TCCGCTCTTAACAGAGTCCCAACCCCATCAATTTACTTCTCTCTCTCTCTCTCTCTCTCTCT 840
Db 1272 TCCGCTCTTAACAGAGTCCCAACCCCATCAATTTACTTCTCTCTCTCTCTCTCTCTCTCTCT 1331
Qy 841 CGTCAAAATAGCAGAACTGAAGTGTCTTCCAGAGGGTCTTCCAGAGCAACCCCTGAG 900
Db 1332 CGTCAAAATAGCAGAACTGAAGTGTCTTCCAGAGGGTCTTCCAGAGCAACCCCTGAG 1391
Qy 901 GTGGATGAAGTGGAGGTGGCTTCTCTCAGGAAACCCCTGGAGCTGTCTGGGAAGCAGATTG 960
Db 1392 GTGGATGAAGTGGAGGTGGCTTCTCTCAGGAAACCCCTGGAGCTGTCTGGGAAGCAGATTG 1451
Qy 961 GAGCAGTGA 969
Db 1452 GAGCAGTGA 1460

RESULT 6

US-09-867-570-3
; Sequence 3, Application US/09867570
; Publication NO. US20040076951A1
; GENERAL INFORMATION:

; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; FILE REFERENCE: CL000900-CIP
; CURRENT APPLICATION NUMBER: US/09/867,570
; CURRENT FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 09/695,045
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; TYPE: DNA
; ORGANISM: Human
; US-09-867-570-3

Query Match 100.0%; Score 969; DB 12; Length 8622;
Best Local Similarity 100.0%; Pred. No. 3.3e-291;
Matches 969; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGATTCAACCATCCAGTCTTGGGTACAGAACTGACCAATCAACGAGCTGAGGAG 60
Db 7528 ATGGATTCAACCATCCAGTCTTGGGTACAGAACTGACCAATCAACGAGCTGAGGAG 7587
Qy 61 ACTCTTGTCTAACAGCAGACCTGAGCTTACGCGGCTGACGTGCATCTGTTCCCTTGTTC 120
Db 7588 ACTCTTGTCTAACAGCAGACCTGAGCTTACGCGGCTGACGTGCATCTGTTCCCTTGTTC 7647
Qy 121 GCGGTGACAGAAACCGGGTGTGCTCTGGCTCTGGCTGCGGCTGCGCATCGCAGAACGCT 180
Db 7648 GCGGTGACAGAAACCGGGTGTGCTCTGGCTCTGGCTGCGGCTGCGCATCGCAGAACGCT 7707
Qy 181 GTCTCCATCTACATCTCTCAACTGGTGGCGGCCGACTTCTCTCTCTAGCGGCCACATT 240
Db 7708 GTCTCCATCTACATCTCTCAACTGGTGGCGGCCGACTTCTCTCTCTAGCGGCCACATT 7767
Qy 241 ATATGTTGCGCGTTACGCTCATCAATATCCGCCATCCCATCTCCAAATCTCTAGTCT 300
Db 7768 ATATGTTGCGCGTTACGCTCATCAATATCCGCCATCCCATCTCCAAATCTCTAGTCT 7827
Qy 301 GTGATGACCTTCT 360
Db 7828 GTGATGACCTTCT 7887
Qy 361 TGCCTGTCCATCTCTGTGCGCCATCTGGTACCACTGCGCGGCCCGCCAGATCTCTCATCG 420
Db 7888 TGCCTGTCCATCTCTGTGCGCCATCTGGTACCACTGCGCGGCCCGCCAGATCTCTCATCG 7947
Qy 421 GTCATGTGTCT 480
Db 7948 GTCATGTGTCT 8007
Qy 481 TGTGACTTCTCTGTGTTAGTGGTGTGATTTCTGTTGGTGTGAAACGTCAGATTTCATTACA 540
Db 8008 TGTGACTTCTCTGTGTTAGTGGTGTGATTTCTGTTGGTGTGAAACGTCAGATTTCATTACA 8067
Qy 541 ATCGCGTGGCTGGTCT 600
Db 8068 ATCGCGTGGCTGGTCT 8127
Qy 601 AGGATTCCTCTGTGGATCCCGAAGATGCGGCTGACCAAGCTGTGACCATCTCTCTCTCTCT 660
Db 8128 AGGATTCCTCTGTGGATCCCGAAGATGCGGCTGACCAAGCTGTGACCATCTCTCTCTCTCT 8187
Qy 661 ACAGTGTGGTCT 720
Db 8188 ACAGTGTGGTCT 8247
Qy 721 AGGATCCACCTGCAATGGAAAGTCTTATTTTGTGTCATGTGTCATCTAGTTTCCATTCTCTG 780
Db 8248 AGGATCCACCTGCAATGGAAAGTCTTATTTTGTGTCATGTGTCATCTAGTTTCCATTCTCTG 8307

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QY 781 TCCGCTCTTAACAGAGTGCACACCCCATCATTTACTTCTCGTGGCTCCCTTTAGGCAG 840
Db 8308 TCCGCTCTTAACAGAGTGCACACCCCATCATTTACTTCTCGTGGCTCCCTTTAGGCAG 8367
QY 841 CFTCAAAATAGGCAGAACCTGAAGCTGGTTCTCCAGAGGGCTCTGCAGGACACGCTGAG 900
Db 8368 CFTCAAAATAGGCAGAACCTGAAGCTGGTTCTCCAGAGGGCTCTGCAGGACACGCTGAG 8427
QY 901 GTGGATGAAGGTGGAGGGTGGCTTCTCAGGAAACCTCGAGCTGTCGGGAAAGCAGATTG 960
Db 8428 GTGGATGAAGGTGGAGGGTGGCTTCTCAGGAAACCTCGAGCTGTCGGGAAAGCAGATTG 8487
QY 961 GAGCAGTGA 969
Db 8488 GAGCAGTGA 8496

RESULT 7
US-10-401-397A-1
; Sequence 1, Application US/10401397A
; Publication No. US20030212001A1
; GENERAL INFORMATION:
; APPLICANT: Pexi, Krishna G.
; APPLICANT: Moffett, Serge
; APPLICANT: Abran, Daniel
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR PREVENTION AND TREATMENT OF ELEVATED
; TITLE OF INVENTION: INTRAOCULAR PRESSURE AND RELATED CONDITIONS
; FILE REFERENCE: 4518/1M674US1
; CURRENT APPLICATION NUMBER: US/10/401,397A
; CURRENT FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: US 60/367,513
; PRIOR FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 969
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(969)
; OTHER INFORMATION: coding sequence for polypeptide
US-10-401-397A-1

Query Match 99.7%; Score 965.8; DB 13; Length 969;
Best Local Similarity 99.8%; Pred. No. 1.2e-290;
Matches 967; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGATTCAACCATCCAGTCTTGGGTACAGAACTGACACCAATCAACGACGAGGAG 60
Db 1 ATGATTCAACCATCCAGTCTTGGGTACAGAACTGACACCAATCAACGACGAGGAG 60
QY 61 ACTCCTTGCTACAAGCAGACCTCGAGCTTACGGGGGTGAGTGCATCGTTTCCCTTGTG 120
Db 61 ACTCCTTGCTACAAGCAGACCTCGAGCTTACGGGGGTGAGTGCATCGTTTCCCTTGTG 120
QY 121 GCGCTGACAGAAACCGGGTGTGCTCTGGCTCTCGGGCTCCGCGATGCCAGGAAGCT 180
Db 121 GCGCTGACAGAAACCGGGTGTGCTCTGGCTCTCGGGCTCCGCGATGCCAGGAAGCT 180
QY 181 GTCTCCATCTACATCTCTCAACCTGGTCCGCGCCGACCTCTCTTCTTCCCTTAGCGGCACATT 240
Db 181 GTCTCCATCTACATCTCTCAACCTGGTCCGCGCCGACCTCTCTTCTTCCCTTAGCGGCACATT 240
QY 241 ATATGTTCCGGTTACGGCTCATCATATATCGCCATCCATCTCCAAATCTCTCAGTCCT 300
Db 241 ATATGTTCCGGTTACGGCTCATCATATATCGCCATCCATCTCTCCAAATCTCTCAGTCCT 300
QY 301 GTGATGACCTTCCCTACTTTATAGGCTTAAGCACTGTAGCGGCATCAGCAGCAGCGC 360
Db 301 GTGATGACCTTCCCTACTTTATAGGCTTAAGCACTGTAGCGGCATCAGCAGCAGCGC 360
QY 361 TGCCTGTCCATCTCTGTGGCCCATCTGTGTPACCACTGCGCGCCGCCCGCCAGATCTGTATCG 420
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Db 361 TGCCTGTCCATCTCTGTGGCCCATCTGTATACACTGCGCGCCGCCCGCCAGATACCTGTATCG 420
QY 421 GTCATGTGTGTCTCTGCTTGGGCCCCCTCTCCCTGCTGCGGAGTATCTCTGGAGTGGATGTTTC 480
Db 421 GTCATGTGTGTCTCTGCTTGGGCCCCCTCTCCCTGCTGCGGAGTATCTCTGGAGTGGATGTTTC 480
QY 481 TGTGACTTCTCTGTTTGTAGTGGTGTGATCTGTTTGTGGTGTGAAAGCTCAGATTTCAATTACA 540
Db 481 TGTGACTTCTCTGTTTGTAGTGGTGTGATCTGTTTGTGGTGTGAAAGCTCAGATTTCAATTACA 540
QY 541 ATCGCGTGGCTGGTGTGTTTATGTGTGTTCTCTGTGGGTCCAGCCCTGGCTCTCTGCTG 600
Db 541 ATCGCGTGGCTGGTGTGTTTATGTGTGTTCTCTGTGGGTCCAGCCCTGGCTCTCTGCTG 600
QY 601 AGGATTTCTGTGGATCCCGGAAGATGCGCGTGCACGAGGCTGTACGTGACCATCTCTCTC 660
Db 601 AGGATTTCTGTGGATCCCGGAAGATGCGCGTGCACGAGGCTGTACGTGACCATCTCTCTC 660
QY 661 ACAGTGTGTGTCTTCCCTCTCTGTGGCTGCCCCCTTGGCATTCAGTGGGCCCCCTGTTTCC 720
Db 661 ACAGTGTGTGTCTTCCCTCTCTGTGGCTGCCCCCTTGGCATTCAGTGGGCCCCCTGTTTCC 720
QY 721 AGGATCCACCTGGATTTGGAAGTCTTATTTTGTGTCATGTGATCTAGTTTCAATTTCTGTG 780
Db 721 AGGATCCACCTGGATTTGGAAGTCTTATTTTGTGTCATGTGATCTAGTTTCAATTTCTGTG 780
QY 781 TCCGCTCTTAACAGCAGTGCACACCCCATCATTTACTTCTTCGTGGGTCTCTTTAGGCAG 840
Db 781 TCCGCTCTTAACAGCAGTGCACACCCCATCATTTACTTCTTCGTGGGTCTCTTTAGGCAG 840
QY 841 CGTCAAAATAGCAGAACCTCAAGTGGTCTCCAGAGGGCTCTGCGAGCACCGCTGAG 900
Db 841 CGTCAAAATAGCAGAACCTCAAGTGGTCTCCAGAGGGCTCTGCGAGCACCGCTGAG 900
QY 901 GTGGATGAAGGTGGAGGGTGGCTTCTCAGGAAACCTCGAGCTGTCGGGAAAGCAGATTG 960
Db 901 GTGGATGAAGGTGGAGGGTGGCTTCTCAGGAAACCTCGAGCTGTCGGGAAAGCAGATTG 960
QY 961 GAGCAGTGA 969
Db 961 GAGCAGTGA 969

RESULT 8
US-10-292-798-1273
; Sequence 1273, Application US/10292798
; Publication No. US20030235833A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 084335/166
; CURRENT APPLICATION NUMBER: US/10/292,798
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 10/017,161
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: JP 2001-246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2070
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1273
; LENGTH: 1369
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; LOCATION: source
; FEATURE:
; LOCATION: (1)..(1369)
; FEATURE:
; NAME/KEY: CDS
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LOCATION: (201)...(1169)
US-10-292-798-1273

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Query Match      99.7%; Score 965.8; DB 16; Length 1369;  
Best Local Similarity 99.6%; Pred. No. 1.4e-290;  
Matches 967; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 ATGGATTCAACCATCCAGTCTTGGGTACAGAACTGACACCAATCAACGAGCGTGAAGAG 60  
DB 201 ATGGATTCAACCATCCAGTCTTGGGTACAGAACTGACACCAATCAACGAGCGTGAAGAG 260  
  
QY 61 ATCTCTGTCTAAGCAGACCTGAGCTTCAGGGGCTGACGTGATGTTCCCTTGTTC 120  
DB 261 ATCTCTGTCTAAGCAGACCTGAGCTTCAGGGGCTGACGTGATGTTCCCTTGTTC 320  
  
QY 121 GGGCTGACAGGAAACGGCGTGTGTCTGGCTCCCTGGCTGCGCATGCGCAGGAACGCT 180  
DB 321 GCGCTGACAGGAAACGGCGTGTGTCTGGCTCCCTGGCTGCGCATGCGCAGGAACGCT 380  
  
QY 181 GTCTCGATCTACATCTCAACCTGATGCTGGGCGGAGCTTCTCTTCTTAGCGGCACATT 240  
DB 381 GTCTCGATCTACATCTCAACCTGATGCTGGGCGGAGCTTCTCTTCTTAGCGGCACATT 440  
  
QY 241 ATATGTTCCCGCTAGCGCTCATCAATATCCGCCATCCCATCTCCAAATCTCTAGTCT 300  
DB 441 ATATGTTCCCGCTAGCGCTCATCAATATCCGCCATCCCATCTCCAAATCTCTAGTCT 500  
  
QY 301 GTGATGACCTTTCCCTTACCTTTATAGCTTAAGCATGCTGAGCGCATCAGCACCGAGCGC 360  
DB 501 GTGATGACCTTTCCCTTACCTTTATAGCTTAAGCATGCTGAGCGCATCAGCACCGAGCGC 560  
  
QY 361 TGCCTGTCCATCTGTGGGCCATCTGGTACCACTGCGCGGCCCGCAGATACCTGTATCG 420  
DB 561 TGCCTGTCCATCTGTGGGCCATCTGGTACCACTGCGCGGCCCGCAGATACCTGTATCG 620  
  
QY 421 GTCATGTGTCTCTGCTCTGGGCCCTGTCTCTGTGGGTCCAGGCTGCTCTGTCTGTC 480  
DB 621 GTCATGTGTCTCTGCTCTGGGCCCTGTCTCTGTGGGTCCAGGCTGCTCTGTCTGTC 680  
  
QY 481 TGTGACTTCCCTTTAGTGGTCTGATCTGTTGGTGTGGAACGTGAGATTTCAATTACA 540  
DB 681 TGTGACTTCCCTTTAGTGGTCTGATCTGTTGGTGTGGAACGTGAGATTTCAATTACA 740  
  
QY 541 ATCGGCTGGCTGGTTTTTTTATGTGTGTCTCTGTGGGTCCAGGCTGCTCTGTCTGTC 600  
DB 741 ATCGGCTGGCTGGTTTTTTTATGTGTGTCTCTGTGGGTCCAGGCTGCTCTGTCTGTC 800  
  
QY 601 AGGATTCCTGTGGATCCCGGAAGATGCGCTGACAGGCTGTAGTGACCATCTCTCTC 660  
DB 801 AGGATTCCTGTGGATCCCGGAAGATGCGCTGACAGGCTGTAGTGACCATCTCTCTC 860  
  
QY 661 ACAGTCTGCTGCTTCTCTCTCTGTGGCTGCGCTTGGCATTCAGTGGGCGCTGTTTTCC 720  
DB 861 ACAGTCTGCTGCTTCTCTCTCTGTGGCTGCGCTTGGCATTCAGTGGGCGCTGTTTTCC 920  
  
QY 721 AGGATCCACTGATTTGGAAGTCTTTATTTGTGATGTCATCTAGTTTCATTTTCTGT 780  
DB 921 AGGATCCACTGATTTGGAAGTCTTTATTTGTGATGTCATCTAGTTTCATTTTCTGT 980  
  
QY 781 TCCGCTCTTAAACAGCAGTGCACACCCCATCATTTACTTCTCTGTGGCTCCTTTAGGCG 840  
DB 981 TCCGCTCTTAAACAGCAGTGCACACCCCATCATTTACTTCTCTGTGGCTCCTTTAGGCG 1040  
  
QY 841 CGTCAAAATAGGCAGAACCTGAGCTGTTCTCCAGAGGCTCTCGACGACACGCTGAG 900  
DB 1041 CGTCAAAATAGGCAGAACCTGAGCTGTTCTCCAGAGGCTCTCGACGACACGCTGAG 1100  
  
QY 901 GTGGATGAAGGTGGAGGTGGCTTCTCTCAGGAAACCTCGAGCTGTGCGGAGACGATTG 960  
DB 1101 GTGGATGAAGGTGGAGGTGGCTTCTCTCAGGAAACCTCGAGCTGTGCGGAGACGATTG 1160  
  
QY 961 GAGCAGTGA 969  
|||||
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DB 1161 GAGCAGTGA 1169

RESULT 9

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US-10-391-074-1  
; Sequence 1, Application US/10391074  
; Publication No. US20040038345A1  
; GENERAL INFORMATION:  
; APPLICANT: Nehls, Michael  
; APPLICANT: Wattler, Frank  
; TITLE OF INVENTION: No. US20040038345A1e1 Human Seven-Transmembrane Receptors  
; FILE REFERENCE: 7705.0008-00-000  
; CURRENT APPLICATION NUMBER: US/10/391,074  
; CURRENT FILING DATE: 2003-03-17  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 969  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-391-074-1
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Query Match 99.5%; Score 964.2; DB 13; Length 969;
Best Local Similarity 99.7%; Pred. No. 3.9e-290;
Matches 966; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1 ATGGATTCAACCATCCAGTCTTGGGTACAGAACTGACACCAATCAACGAGCGTGAAGAG 60  
DB 1 ATGGATTCAACCATCCAGTCTTGGGTACAGAACTGACACCAATCAACGAGCGTGAAGAG 60  
  
QY 61 ACTCCTTGTCTACAGCAGACCCCTGAGCTTCACGGGGCTGACGTGCATCGTTTCCCTTGT 120  
DB 61 ACTCCTTGTCTACAGCAGACCCCTGAGCTTCACGGGGCTGACGTGCATCGTTTCCCTTGT 120  
  
QY 121 GCGCTGACAGAAACGGCGTGTGTCTGTGCTCTCTGGCTGCGCGCATGCGCAGGAACGCT 180  
DB 121 GCGCTGACAGAAACGGCGTGTGTCTGTGCTCTCTGGCTGCGCGCATGCGCAGGAACGCT 180  
  
QY 181 GTCTCCATCTACATCTCTCAACCTGCTGCGGCGCATCTTCTCTTCTTACGCGCACATT 240  
DB 181 GTCTCCATCTACATCTCTCAACCTGCTGCGGCGCATCTTCTCTTCTTACGCGCACATT 240  
  
QY 241 ATATGTTGCGCGTGTAGCGCTCATCAATATCCGCCATCCCATCTCCAAATCTCTCACTCT 300  
DB 241 ATAGCTTCCGCGTGTAGCGCTCATCAATATCCGCCATCCCATCTCCAAATCTCTCACTCT 300  
  
QY 301 GTGATGACCTTCCCTACTTTATAGGCTTAAGCATGCTGAGCGCATCAGCACCGAGCGC 360  
DB 301 GTGATGACCTTCCCTACTTTATAGGCTTAAGCATGCTGAGCGCATCAGCACCGAGCGC 360  
  
QY 361 TGCCTGTCCATCTCTGTGGGCCATCTGTGTACCACTGCGCGGCCGCCAGATACCTGTCTATCG 420  
DB 361 TGCCTGTCCATCTCTGTGGGCCATCTGTGTACCACTGCGCGGCCGCCAGATACCTGTCTATCG 420  
  
QY 421 GTCATGTGTCTCTGCTCTGGGCCCTGTCTCTCTCTGCGGAGTATCTTGGAGTGTGATGTT 480  
DB 421 GTCATGTGTCTCTGCTCTGGGCCCTGTCTCTCTCTGCGGAGTATCTTGGAGTGTGATGTT 480  
  
QY 481 TGTGACTTCCCTTTAGTGGTGTGATTTCTTTGTGTGTAACCGTGCAGATTTTCAATTACA 540  
DB 481 TGTGACTTCCCTTTAGTGGTGTGATTTCTTTGTGTGTAACCGTGCAGATTTTCAATTACA 540  
  
QY 541 ATCCGCTGGCTGGTTTTTTTATGTGTGGTCTCTGTGGGTCCAGCTGCTGCTGCTGCT 600  
DB 541 ATCCGCTGGCTGGTTTTTTTATGTGTGGTCTCTGTGGGTCCAGCTGCTGCTGCTGCTGCT 600  
  
QY 601 AGGATTCCTGTGTGATCCCGGAAGATGCGCTGACAGGCTGTACGTCGACCATCTCTCTC 660  
DB 601 AGGATTCCTGTGTGATCCCGGAAGATGCGCTGACAGGCTGTACGTCGACCATCTCTCTC 660  
  
QY 661 ACAGTGTGTGCTTCTCTCTCTGTGGCTCTCTGTGGCTCTCTGTGGCTCTCTGTGGCTCT 720  
DB 661 ACAGTGTGTGCTTCTCTCTCTGTGGCTCTCTGTGGCTCTCTGTGGCTCTCTGTGGCTCT 720
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QY 721 AGGATCCACCTGGATTGGAAGTCTTATTTTGTGATGTGATCTAGTTTCCATTTTCCTG 780
Db 721 AGGATCCACCTGGATTGGAAGTCTTATTTTGTGATGTGATCTAGTTTCCATTTTCCTG 780
QY 781 TCCGCTCTTAACAGCAGTGCACCCCATCATTTACTTCTTGTGGGCTCTTTTAGGCAG 840
Db 781 TCCGCTCTTAACAGCAGTGCACCCCATCATTTACTTCTTGTGGGCTCTTTAGGCAG 840
QY 841 CGTCAAAATAGGCAAGACCTGAAGCTGGTCTCCAGAGGCTCTGAGGACAGCCTGAG 900
Db 841 CGTCAAAATAGGCAAGACCTGAAGCTGGTCTCCAGAGGCTCTGAGGACAGCCTGAG 900
QY 901 GTGGATGAAGTGGAGGCTGGCTTCCCTCAGAAACCTGTGAGCTGTGCGGAAGCAGATTG 960
Db 901 GTGGATGAAGTGGAGGCTGGCTTCCCTCAGAAACCTGTGAGCTGTGCGGAAGCAGATTG 960
QY 961 GAGCAGTGA 969
Db 961 GAGCAGTGA 969

RESULT 10
US-10-237-467-9
; Sequence 9, Application US/10237467
; Publication No. US20030186324A1
; GENERAL INFORMATION:
; APPLICANT: Liao, Jiayu
; APPLICANT: Gray, Nathanael S.
; APPLICANT: Caldwell, Jeremy C.
; APPLICANT: Schultz, Peter G.
; APPLICANT: IRM LLC
; TITLE OF INVENTION: Sensory Neuron Receptors
; FILE REFERENCE: 021288-001300US
; CURRENT APPLICATION NUMBER: US/10/237,467
; CURRENT FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: US 60/317,879
; PRIOR FILING DATE: 2001-09-07
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 9
; LENGTH: 909
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: dorsal root ganglia G-protein coupled receptor (GPCR)
US-10-237-467-9

Query Match 87.3%; Score 845.8; DB 15; Length 909;
Best Local Similarity 99.8%; Pred. No. 3.5e-253;
Matches 847; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 121 GCGGTGACAGAAACGCGGTTGTGCTCTGGCTCTGGGCTGCCCATGCGCAGGAACGCT 180
Db 61 GCGGTGACAGAAACGCGGTTGTGCTCTGGCTCTGGGCTGCCCATGCGCAGGAACGCT 120
QY 191 GTCTCCATCTACATCTCAACCTGTGCGCGCGACTTCTCTTCTTAGCGGCCACATT 240
Db 121 GTCTCCATCTACATCTCAACCTGTGCGCGCGACTTCTCTTCTTAGCGGCCACATT 180
QY 241 ATATGTTCCGCTTACGCTCATCAATATCCGCCATCCCATCTCCAAAATCTCTCAGTCT 300
Db 191 ATATGTTCCGCTTACGCTCATCAATATCCGCCATCCCATCTCCAAAATCTCTCAGTCT 240
QY 301 GTGATGACCTTCTCCCTACTTATAGGCTTAGCATGTGAGCGGCATCAGCAGCCGAGCGC 360
Db 241 GTGATGACCTTCTCCCTACTTATAGGCTTAGCATGTGAGCGGCATCAGCAGCCGAGCGC 300
QY 361 TGCCTGTCCATCTCTGCGCCCATCTGTGTAACCACTGCGCGCCGCCCCAGATACCTGTATCG 420
Db 301 TGCCTGTCCATCTCTGCGCCCATCTGTGTAACCACTGCGCGCCGCCCCAGATACCTGTATCG 360

RESULT 11

US-09-995-225-17
; Sequence 17, Application US/09995225
; Publication No. US20020193584A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Chu, Zhi Liang
; APPLICANT: Dang, Huang T.
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Pride, Cameron
; TITLE OF INVENTION: Endogenous And No. US20020193584A1-Endogenous Versions of Human
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0308
; CURRENT APPLICATION NUMBER: US/09/995,225
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: PCT/US99/23938
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/253,404
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/255,366
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/270,286
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/282,365
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/270,266
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/282,032
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,358

QY 421 GTCATGTGTCTGCTCTGGCCCTGTCCTGTCGGAGTATCTCTGGAGTGATGTTTC 480
Db 361 GTCATGTGTCTGCTCTGGCCCTGTCCTGTCGGAGTATCTCTGGAGTGATGTTTC 420
QY 481 TGTGACTTCTCTGTTTGTAGTGTGCTGATTTCTGTTTGGTGTGAAACGTGAGATTTTCATTACA 540
Db 421 TGTGACTTCTCTGTTTGTAGTGTGCTGATTTCTGTTTGGTGTGAAACGTGAGATTTTCATTACA 480
QY 541 ATCCGGTGGCTGGTTTTTATGTGTGTTCTCTGTGGTCCAGCCTGGTCTCTGCTGTC 600
Db 481 ATCCGGTGGCTGGTTTTTATGTGTGTTCTCTGTGGTCCAGCCTGGTCTCTGCTGTC 540
QY 601 AGGATTTCTCTGTGGATCCCGAAGATCCGCTGACCAAGGCTGTACGTACCATCTCTCTC 660
Db 541 AGGATTTCTCTGTGGATCCCGAAGATCCGCTGACCAAGGCTGTACGTACCATCTCTCTC 600
QY 661 ACAGTGTGCTTCTCTCTCTCTGTGGCTGCCCTTGTGCATTGAGTGGCCCTGTTTTTC 720
Db 601 ACAGTGTGCTTCTCTCTCTCTGTGGCTGCCCTTGTGCATTGAGTGGCCCTGTTTTTC 660
QY 721 AGGATCCACCTGGATTGGAAGTCTTATTTTGTGATGTGATCTAGTTTCCATTTTCCTG 780
Db 661 AGGATCCACCTGGATTGGAAGTCTTATTTTGTGATGTGATCTAGTTTCCATTTTCCTG 720
QY 781 TCCGCTCTTAACAGCAGTGCACCCCATCATTTACTTCTCTGGGCTCTCTTTAGGCAG 840
Db 721 TCCGCTCTTAACAGCAGTGCACCCCATCATTTACTTCTCTGGGCTCTCTTTAGGCAG 780
QY 841 CGTCAAAATAGGCAAGACCTGAAGCTGGTCTCTCAGAGGCTCTGCGAGACACGCTGAG 900
Db 781 CGTCAAAATAGGCAAGACCTGAAGCTGGTCTCTCAGAGGCTCTGCGAGACACGCTGAG 840
QY 901 GTGGATGAAGTGGAGGCTGGCTTCCCTCAGAAACCTGTGAGCTGTGCGGAAGCAGATTG 960
Db 841 GTGGATGAAGTGGAGGCTGGCTTCCCTCAGAAACCTGTGAGCTGTGCGGAAGCAGATTG 900
QY 961 GAGCAGTGA 969
Db 901 GAGCAGTGA 909

; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,356
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/290,917
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/309,208
; PRIOR FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 17
; LENGTH: 969
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. US20020193584A1el Sequence
US-09-995-225-17

Query Match 86.0%; Score 833; DB 9; Length 969;
Best Local Similarity 91.2%; Pred. No. 3.6e-249;
Matches 884; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

QY 1 ATGGATTCAACCATCCAGTCTTGGGTACAGAACTGACACCAATCAACGGAGCTGAGGAG 60
DB 1 ATGGATTCAACCATCCAGTCTTGGGTACAGAACTGACACCAATCAACGGAGCTGAGGAG 60
QY 61 ACTCCTTGCTACAAAGCAGACCCCTGAGCTTACGGGCTGACGTGCATCGTTTCCCTTGTG 120
DB 61 ACTCCTTGCTACAAATCAGACCCCTGAGCTTACGGGCTGACGTGCATCGTTTCCCTTGTG 120
QY 121 GGGTACAGAGAAACGGGTTGTCTGGCTCTGGGCTCGCGGCTCGGATCGGAGAACGCT 180
DB 121 GGAATACAGAGAAACGGGTTGTCTGGCTCTGGGCTCGCGGCTCGGATCGGAGAACGCT 180
QY 181 GTCTCCATCTACATCTCAACCTGTGGGCGGCTTCTCTCTCTTAGCGGCCACATT 240
DB 181 GTCTCCATCTACATCTCAACCTGTGGGCGGCTTCTCTCTCTTAGCGGCCACATT 240
QY 241 ATATGTTCCGGTTAGCTCTATCAATATCCGCAATCCCATCTCCAAATCTCTAGTCT 300
DB 241 ATAGTTTCGCCATTAGCTCTATCAATATCCGCAATCTCATCCGCAAAATCTCTAGTCT 300
QY 301 GTGATGACCTTCCCTTACTTTATAGGCTTAAGCCTAAGCATGCTGAGCGCCATCAGCACCGGCG 360
DB 301 GTGATGACCTTCCCTTACTTTATAGGCTTAAGCCTAAGCATGCTGAGCGCCATCAGCACCGGCG 360
QY 361 TGCTGTCCATCTGTGGGCCCATCTGGTACCACTGCGCGGCCGCCAGATACCTGTCTATCG 420
DB 361 TGCTGTCTGTCTGTGGGCCCATCTGGTACCGCTGCGCGGCCGCCACACACCTGTCTAGCG 420
QY 421 GTCATGTGTCTGTCTGGGCCCTGTCCCTGCTGCGGAGTATCTGGAGTGGATGTC 480
DB 421 GTGATGTGTCTGTCTGGGCCCTGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
QY 481 TGTGACTTCTGTTTGTGTTAGTGGTGTGATTTCTGTTTGGTGTGAACCTGACAGATTTCATTACA 540
DB 481 TGTGACTTCTGTTTGTGTTAGTGGTGTGATTTCTAGTGTGTGAACCTGACAGATTTCATTCCA 540
QY 541 ATCGGTGTGCTGTTTTTTTATGTGTGTGTCTGTGGGTTCAGCGCTGCTGCTGCTGCTGCTGCTG 600
DB 541 GTGCGGTGTGCTGTTTTTTTATGTGTGTGTCTGTGGGTTCAGCGCTGCTGCTGCTGCTGCTGCTG 600
QY 601 AGGATCTCTGTGGATCCCGGAGATGCGGCTGACCGAGCTGTAGTGCACCATCTCTCTC 660
DB 601 AGGATCTCTGTGGATCCCGGAGATGCGGCTGACCGAGCTGTAGTGCACCATCTCTCTC 660
QY 661 ACAGTGTGGTCTTCTCTCTGTGGCTCGCCCTTGGCAATTCAGTGGGCCCTGTTTCC 720
DB 661 ACAGTGTGGTCTTCTCTCTGTGGCTCGCCCTTGGCAATTCAGTGGGCCCTGTTTCC 720
QY 721 AGGATCCACTGATTTGGAAGCTTTATTTTGTGATGCTCATCTAGTTTCCATTTCTG 780
DB 721 AGGATCCACTGATTTGGAAGCTTTATTTTGTGATGCTCATCTAGTTTCCATTTCTG 780

QY 781 TCCGCTCTTAACAGAGTGCACAAACCCCATCATTTACTTCTTCTGGGCTCCTTTAGGCAG 840
DB 781 TCCCTCTCTAAACAGTAGTGCACAAACCCCATCATTTACTTCTTCTGGGCTCCTTTAGGCAG 840
QY 841 CGTCAAAATAGGACAGACCTGAAGCTGTTTCTCCAGAGGCTCTGAGGACACGCTTGTAG 900
DB 841 CGTCAAAATAGGACAGACCTGAAGCTGTTTCTCCAGAGGCTCTGAGGACACGCTTGTAG 900
QY 901 GTGGATCAAGGTGAGGGTGGCTTCTCAGAAACCTCGAGTGTGCGGAAGCAGATTG 960
DB 901 GTGGATAAAGGTGAAGGGCAGCTTCTCAGAAAGCTCGAGTGTGCGGAAGCAGATTG 960
QY 961 GAGCAGTGA 969
DB 961 GGGCCATGA 969

RESULT 12
US-09-995-225-17
; Sequence 17, Application US/09995225
; Publication No. US20030139588A9
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Chu, Zhi Liang
; APPLICANT: Dang, Huong T.
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Pride, Cameron
; TITLE OF INVENTION: Endogenous And No. US20030139588A9- Endogenous Versions of Human
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0308
; CURRENT APPLICATION NUMBER: US/09/995,225
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: PCT/US99/23938
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/253,404
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/255,366
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/270,286
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/282,365
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/270,266
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/282,032
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,358
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,356
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/290,917
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/309,208
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 17
; LENGTH: 969
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. US20030139588A9el Sequence
US-09-995-225-17

Query Match 86.0%; Score 833; DB 10; Length 969;
Best Local Similarity 91.2%; Pred. No. 3.6e-249;
Matches 884; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

QY 1 ATGGAATCAACCATCCAGTCTTGGGTACAGAACTGACACCAATCAACGGAGCTGAGGAG 60
DB 1 ATGGAATCAACCATCCAGTCTTGGGTACAGAACTGACACCAATCAACGGAGCTGAGGAG 60

QY 61 ACTCCTTGCTACAGCAGACCCCTGAGCTTCACGGGGCTGACGTCATCGTTTCCCTTGTTC 120
Db |||||
QY 61 ACTCCTTGCTACAAATCAGACCCCTGAGCTTCACGGTGTGCTGACGTGATCATTTCCCTTGTTC 120
Db |||||
QY 121 GGGCTGACAGGAAACCGGCTGTGCTGCTGCTTCTGGCTTCTGGGCTGCGCATGCGAGGAAACGCT 180
Db |||||
QY 121 GAGTACAGGAAACCGGCTGTGCTGCTGCTTCTGGCTTCTGGGCTACCGCATGCGAGGAAACGCT 180
Db |||||
QY 181 GTCTCCATCTACATCCTCAACCTGTGCTGGGGCTGCTTCTTCTTCTTCTAGGGCCACATTT 240
Db |||||
QY 181 GTCTCCATCTACATCCTCAACCTGTGCTGGGGCTGCTTCTTCTTCTTCTAGGGCTTCCAGATT 240
Db |||||
QY 241 ATATGTTTCCGCTTACGCTCTCATCAATATCCGCCATCCCATCTCCAAATCTCTAGTCTCT 300
Db |||||
QY 241 ATAGCTTCCGCTTACGCTCTCATCAATATCCGCCATCTCTCCAAATCTCTAGTCTCT 300
Db |||||
QY 301 GTGATGACCTTCTCCCTTACCTTTATAGGCTTATAGGCTTATAGGCTTATAGGCTTATAGGCT 360
Db |||||
QY 301 GTGATGACCTTCTCCCTTACCTTTATAGGCTTATAGGCTTATAGGCTTATAGGCTTATAGGCT 360
Db |||||
QY 361 TGGCTGTCCATCTGCTGGGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Db |||||
QY 361 TGGCTGTCCATCTGCTGGGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Db |||||
QY 421 GTCATGTGTCTCTGCTTCTGGGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
Db |||||
QY 421 GTCATGTGTCTCTGCTTCTGGGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
Db |||||
QY 481 TGTGACTTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
Db |||||
QY 481 TGTGACTTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
Db |||||
QY 541 ATCGCTGCTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
Db |||||
QY 541 ATCGCTGCTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
Db |||||
QY 601 AGGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
Db |||||
QY 601 AGGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
Db |||||
QY 661 ACAGTGTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
Db |||||
QY 661 ACAGTGTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
Db |||||
QY 721 AGGATCACCCTGATTTGGAAAGCTCTTATTTTGTGATGTCATCTAGTTTCCATTTTCTG 780
Db |||||
QY 721 AGGATCACCCTGATTTGGAAAGCTCTTATTTTGTGATGTCATCTAGTTTCCATTTTCTG 780
Db |||||
QY 781 TCCGCTCTTAACAGCAGTGCACCCCATCATTTACTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
Db |||||
QY 781 TCCGCTCTTAACAGCAGTGCACCCCATCATTTACTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
Db |||||
QY 841 CGTCAAAATAGGCAAGACCTGAGCTGCTTCTGAGAGGCTTCTGAGAGGCTTCTGAGAGGCTTCTGAGAG 900
Db |||||
QY 841 CGTCAAAATAGGCAAGACCTGAGCTGCTTCTGAGAGGCTTCTGAGAGGCTTCTGAGAGGCTTCTGAGAG 900
Db |||||
QY 901 GTGATGAGGCTGAGGCTGCTTCTGAGAGGCTTCTGAGAGGCTTCTGAGAGGCTTCTGAGAGGCTTCTGAG 960
Db |||||
QY 901 GTGATGAGGCTGAGGCTTCTGAGAGGCTTCTGAGAGGCTTCTGAGAGGCTTCTGAGAGGCTTCTGAGAG 960
Db |||||
QY 961 GAGCAGTGA 969
Db |||||
QY 961 GGGCCATGA 969
Db |||||

RESULT 13
US-10-237-467-3
; Sequence 3, Application US/10237467
; Publication No. US20030186324A1
; GENERAL INFORMATION:
; APPLICANT: Liao, Jiayu
; APPLICANT: Gray, Nathanael S.

; APPLICANT: Caldwell, Jeremy C.
; APPLICANT: Schultz, Peter G.
; APPLICANT: IRM LLC
; TITLE OF INVENTION: Sensory Neuron Receptors
; FILE REFERENCE: 021288-001300US
; CURRENT APPLICATION NUMBER: US/10/237,467
; CURRENT FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: US 60/317,879
; PRIOR FILING DATE: 2001-09-07
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 3
; LENGTH: 969
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: dorsal root ganglia G-protein coupled receptor (GPCR)
; OTHER INFORMATION: 2 (DRG2) (X2HTBL3EYAW)
; US-10-237-467-3

Query Match 86.0%; Score 833; DB 15; Length 969;
Best Local Similarity 91.2%; Pred. No. 3.6e-249;
Matches 884; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

QY 1 ATGATTTCAACCACTCCAGTCTTGGGTACAGAACTGACACCAATCAACGAGCGTGGAGG 60
Db 1 ATGATTTCAACCACTCCAGTCTTGGGTACAGAACTGACACCAATCAACGAGCGTGGAGG 60
QY 61 ACTCCTTGCTACAGCAGACCCCTGAGCTTCAACGGGGCTGACGTCATCGTTTCCCTTGTTC 120
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QY 121 GCGCTGACAGGAAACGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
Db 121 GCGCTGACAGGAAACGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
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Db 241 ATATGTTTCCGCTTACGCTCTCATCAATATCCGCCATCCCATCTCCAAATCTCTAGTCTCT 300
QY 301 GTGATGACCTTCTCCCTTACCTTTATAGGCTTATAGGCTTATAGGCTTATAGGCTTATAGGCT 360
Db 301 GTGATGACCTTCTCCCTTACCTTTATAGGCTTATAGGCTTATAGGCTTATAGGCTTATAGGCT 360
QY 361 TGGCTGTCCATCTGCTGGGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Db 361 TGGCTGTCCATCTGCTGGGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
QY 421 GTCATGTGTCTCTGCTTCTGGGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
Db 421 GTCATGTGTCTCTGCTTCTGGGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
QY 481 TGTGACTTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
Db 481 TGTGACTTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
QY 541 ATCGCTGCTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
Db 541 ATCGCTGCTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
QY 601 AGGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
Db 601 AGGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
QY 661 ACAGTGTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
Db 661 ACAGTGTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
QY 721 AGGATCACCCTGATTTGGAAAGCTCTTATTTTGTGATGTCATCTAGTTTCCATTTTCTG 780

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Db 721 AGGATGACCTGAAATTTGGAAGTCTTATATGTTCATGTTTATCTGGTTGATGTCCTG 780
Qy 781 TCCGCTCTTAACAGCAGTGCCAAACCCCATCATTTTACTTCTTCGTGGGCTCCTTTAGGCAG 840
Db 781 TCCCTCTCTAACAGTAGTGCCAAACCCCATCATTTTACTTCTTCGTGGGCTCCTTTAGGCAG 840
Qy 841 CGTCAAAATAGGCGAGAACCTGAAGCTGTTTCTCAGAGGGCTCTGCGAGGACACGCCCTGAG 900
Db 841 CGTCAAAATAGGCGAGAACCTGAAGCTGTTTCTCAGAGGGCTCTGCGAGGACACGCCCTGAG 900
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Qy 961 GAGCAGTGA 969
Db 961 GGGCCATGA 969

RESULT 14
US-10-292-798-1041
; Sequence 1041, Application US/10292798
; Publication No. US20030235833A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 084335/166
; CURRENT APPLICATION NUMBER: US/10/292,798
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 10/017,161
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: JP 2001-246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2070
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1041
; LENGTH: 1369
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; LOCATION: source
; FEATURE:
; LOCATION: (1)..(1369)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (201)..(1169)
US-10-292-798-1041

Query Match 86.0%; Score 833; DB 16; Length 1369;
Best Local Similarity 91.2%; Pred. No. 4,1e-249;
Matches 884; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

Qy 1 ATGGATTCAACCATCCAGCTTCGGTACAGAACTGACACCAATCAACGGACGTGAGGAG 60
Db 201 ATGGATCCAAACCGTCCAGCTTCGGTACAAAACCTGACCAATCAACGGACGTGAGGAG 260
Qy 61 ACTCCTTGCTACAAGCAGACCCCTGAGCTTCACGGGGCTGACGTGATCGTTTCCCTTGTC 120
Db 261 ATCTCTTGCTACAATCAGACCCCTGAGCTTCACGGGTGCTGACGTGATCATTTCCCTTGTC 320
Qy 121 GCGCTGACAGGAAACCGGGTTGTCTTCGGCTTCCTGGGCTGCGGATCGGAGGAAACGCT 180
Db 321 GGAAGTACAGGAAACCGGGTTGTCTTCGGCTTCCTGGGCTACCGGATCGGAGGAAACGCT 380
Qy 181 GTCCTCATCTACATCTCAACTGGTTCGGGGCGGACTTCTCTTCTTCTTAGCGGCCACATT 240
Db 381 GTCCTCATCTACATCTCAACTGGTTCGGGGCGGAGACTTCTCTTCTTCTTAGCGATT 440
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Db 441 ATACGTTTCCCATAGCCTCATCAATATACCCATCTCATCCGAAATCTCGTTTCT 500
Qy 301 GTGATGACCTTCCCTACTTTATAGCCCTTAAGCATGCTAGGCGCCATCAGCACCGAGCC 360
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Qy 361 TGCCTGTCCATCTGTGGGCCATCTGGTACACTGCGCGCGCCGAGTACCTGATCATG 420
Db 561 TGCCTGTCTGTTCTGTGGCCCATCTGGTACCCGCTGCGCGCGCCGAGTACCTGATCATG 620
Qy 421 GTCATGTGTCTGTCTGTGGGCCCTGTCTCCCTGCTGCGGAGTATCTCTGAGTGGATGTC 480
Db 621 GTCGTGTGTCTGTCTGTGGGCCCTGTCTCCCTGCTGCTGTTTAGTATGCTGAGTGGAGTTC 680
Qy 481 TGTGACTTCTGTGTGTAGTGGTCTGATTTCTGTTTGGTGTGTAACCTGAGATTTTATTACA 540
Db 681 TGTGACTTCTGTGTGTAGTGGTCTGATTTCTGTTTGGTGTGTAACCTGAGATTTTATTACA 740
Qy 541 ATCGGTGCTGCTGTTTTTTTATGTGTGGTTCCTGTGGGTCCAGCTGCTGCTGTGTC 600
Db 741 GTCCGTGCTGATTTTTTTTATGTGTGGTTCCTGTGTGTTCCAGCTGCTGCTGTGTC 800
Qy 601 AGGATTTCTGTGGATCCCGGAAGATGCGCTGAGCCAGCTGTACGTGACCATCTCTCTC 660
Db 801 AGGATCTCTGTGGATCCCGGAAGATGCGCTGAGCCAGCTGTACGTGACCATCTCTCTC 860
Qy 661 ACAGTCTGCTCTTCTCTCTCTCTGTGGCTGCTCTTGGCATTCAGTGGGCCCTGTTTCT 720
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Qy 721 AGGATCCACTGGATTTGGAAGTCTTATTTGTCTGATGTCATCTAGTTTCCATTTTCTCTG 780
Db 921 AGGATGCACTGAATTTGGAAGTCTTATATTTGTCTGATGTTTATCTGTTTTCATGCTGCTG 980
Qy 781 TCCGCTCTTAACAGCAGTGCCTCAACCCCATCATTTTCTCTGCTGGGCTCTTTTAGGCAG 840
Db 981 TCCTCTCTAAACAGTAGTGTCCAAACCCCATCATTTTCTCTGTTGGGCTCTTTTAGGCAG 1040
Qy 841 CGTCAAAATAGGCGAGAACCTGAAAGCTGTTCTCCAGAGGGCTCTGCGAGACGCTGAG 900
Db 1041 CGTCAAAATAGGCGAGAACCTGAAAGCTGTTCTCCAGAGGGCTCTGCGAGACGCTGAG 1100
Qy 901 GTGGATGAAGGTGAGGGGTGCTTCCTCAGGAAACCCCTGAGGCTGTCGGGAGCAGATTG 960
Db 1101 GTGGATGAAGGTGAGGGGAGCTTCTGAGGAAAGCTTCTGAGGAAAGCTGCGGAGCAGATTG 1160
Qy 961 GAGCAGTGA 969
Db 1161 GGGCCATGA 1169

RESULT 15
US-10-183-116-32
; Sequence 32, Application US/10-83116
; Publication No. US20030092035A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David J.
; APPLICANT: Dong, Xinzhong
; APPLICANT: Zylka, Mark
; APPLICANT: Simon, Melvin
; APPLICANT: Han, Sang-kyou
; TITLE OF INVENTION: PAIN SIGNALING MOLECULES
; FILE REFERENCE: CALTE 4C1P1
; CURRENT APPLICATION NUMBER: US/10/183,116
; CURRENT FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: US 60/222,344
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: US 60/202,027
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 09/704,707
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/285,493
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; PRIOR FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 09/849,869
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 1604
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (433)...(1398)
US-10-183-116-32

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Query Match		86.0%;	Score 833;	DB 15;	Length 1604;
Best Local Similarity		91.2%;	Pred. No. 4,4e-249;		
Matches 884;		Conservative 0;	Mismatches 85;	Indels 0;	Gaps 0;
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QY	61	ACTCCTTGCTACAGAGACCCCTGAGCTTCACGGGGCTGACGGTATCGTTCCCTTGTG	120		
Db	493	ACTCCTTGCTACAAATCAGACCCCTGAGCTTCACGGGGCTGACGGTATCGTTCCCTTGTG	552		
QY	121	GGGCTGACAGGAAACCGGTTGTCTCTGGCTCTGGGCTGCCGATGCCAGGAACGCT	180		
Db	553	GGAGCTGACAGGAAACCGGTTGTCTCTGGCTCTGGGCTGCCGATGCCAGGAACGCT	612		
QY	181	GTCTCCATCTACATCCTCAACCTGTGGGGCGGAGTTCCTCTCTTAGCGGCCACATT	240		
Db	613	GTCTCCATCTACATCCTCAACCTGTGGGGCGGAGTTCCTCTCTTAGCGGCCACATT	672		
QY	241	ATATGTTCCGCGTTAGCCCTCATCAATATCCGCCATCCCATCTCCAAATCTCTAGTCT	300		
Db	673	ATAGCTTCGCCATTACGCCCTCATATACGCCATCTCATCCGCAAAATCTCTGTTCT	732		
QY	301	GTGATGACCTTTCCCTACTTTATAGCCCTAAGATGCTGAGCGCCATCAGCACCGAGCGC	360		
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QY	361	TGCGTGTCCATCTGTGGGCCATCTGTACCACTGCGCGGCCCCAGATACCTGTCACTCG	420		
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QY	421	GTCAATGATGCTCTGCTGGGCCCTGTCCCTGCTGCGGAGTATCCTGAGTGGATGTTTC	480		
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QY	481	TGTGACTTCTGTTAGTGGTGTGATTTCTGTTTGGTGTGAACGTCAGATTTCAATACA	540		
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QY	541	ATCGCGTGGCTGTTTTTTTATGTGGTCTCTGTGGGTCCAGCTGTCTGTGGTTC	600		
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QY	601	AGGATCTCTGTGGATCCCGAGATGCCGCTGACAGGCTGTACGTGACCATCTCTCTC	660		
Db	1033	AGGATCTCTGTGGATCCCGAGATGCCGCTGACAGGCTGTACGTGACCATCTCTCTC	1092		
QY	661	ACAGTGTGCTCTCTCTCTCTCTGCTGGGCTGCCCTTTGGCATTCAGTGGGCCCTGTTTCC	720		
Db	1093	ACAGTGTGCTCTCTCTCTCTCTGCTGGGCTGCCCTTTGGCATTCAGTGGGCCCTGTTTCC	1152		
QY	721	AGGATCCACTGATTTGGAAGTCTTATTTTGTGCTGATCTAGTATTCATTTTCTCTG	780		
Db	1153	AGGATCCACTGATTTGGAAGTCTTATTTTGTGCTGATTTTATTTGCTGATTTTCTCTG	1212		
QY	781	TCCGCTCTTAACAGACGTGCCACCCCATCATTTACTTCTTCGTGGGCTCTTTAGGCAG	840		
Db	1213	TCCGCTCTTAACAGACGTGCCACCCCATCATTTACTTCTTCGTGGGCTCTTTAGGCAG	1272		

Search completed: July 4, 2004, 08:42:22
Job time : 528 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 4, 2004, 05:06:47 ; Search time 3093 Seconds
(without alignments)
9355.465 Million cell updates/sec

Title: US-09-787-879C-3

Perfect score: 969

Sequence: 1 atggattcaaccatccagc.....gaagcagattggagcagtgga 969

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: em_esthum:*

3: em_estin:*

4: em_estnu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_esti:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	559.8	57.8	688	10	B439409
4	548.2	56.6	757	12	BG208126

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	6	457.2	47.2	924	14	CD051096
	7	358.8	37.0	503	28	AQ888076
	8	347	35.8	468	28	B74348
	9	343	35.4	2075	11	AK029369
	10	335.4	34.6	620	28	AQ696198
	11	297.4	30.7	905	14	CD243595
	12	285.6	29.5	618	12	B1828553
	13	284.6	29.4	704	13	B741352
	14	279.8	28.9	783	14	CD469424
	15	279.2	28.8	515	9	AL705589
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	17	274	28.3	770	14	CD469131
	18	273.8	28.3	777	14	CD467625
	19	273.2	28.2	576	14	CD469125
	20	272.6	28.1	725	14	CD468987
	21	272.6	28.1	761	14	CD467287
	22	270.8	27.9	719	14	CD469292
	23	270.2	27.9	503	9	AF003828
	24	264.8	27.3	756	14	CD469433
C	25	262	27.0	682	28	A2346449
	26	242.2	25.0	639	14	CD467510
	27	241.2	24.9	634	14	CD471204
	28	241.2	24.9	634	14	CD471217
	29	241.2	24.9	644	14	CD469330
	30	239.6	24.7	637	14	CD467799
	31	237.6	24.5	644	14	CD470186
	32	235.4	24.3	630	14	CD470076
	33	230	23.7	767	14	CD467920
	34	229.2	23.7	634	14	CD535184
	35	229	23.6	618	14	CD470897
	36	228.4	23.6	664	14	CD535223
	37	228.4	23.6	669	14	CD535616
	38	228	23.5	621	14	CD470214
	39	227.6	23.5	704	13	BY741329
	40	227	23.4	515	28	A2602580
	41	222	22.9	733	13	BY741303
	42	219.4	22.6	484	10	BB853701
	43	217	22.4	633	14	CD470991
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ALIGNMENTS

RESULT 1
CA455045
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

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AGENCOURT_10735784 MAPcL Homo sapiens cDNA clone IMAGE:6722551 5',
889 bp mRNA linear EST 12-NOV-2002
RNA sequence.
CA455045
CA455045.1 GI:24905369
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 889)
NIH-MGC Institutes of Health, Mammalian Gene Collection (MGC)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: sgabbs@mail.nih.gov
Tissue Procurement: Kristi A. Egland, Ira Pastan
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM14265 row: h column: 07
High quality sequence stop: 743.

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		/note="Vector: pCMV-SPORT6; Site 1: EcoRV; Site 2: Not I; Subtracted with brain, liver, lung, kidney and muscle. Directionally cloned. Priming method: oligo-dT. Average insert size: 1800 bp. Library amplification: 26,000 fold. Kristi A. Eglund, James J. Vincent, Robert Strausberg, Bungkok Lee & Ira Pastan: Discovery of new breast cancer genes encoding membrane and secreted proteins. Manuscript submitted."	
ORIGIN		70.4%; Score 682.2; DB 14; Length 889;	
Query Match		97.8%; Pred. No. 1.2e-149;	
Best Local Similarity		701; Conservative 0; Mismatches 15; Indels 1; Gaps 1;	
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QY	61	ACTCCTGCTACAGAGACCCCTGAGCTTACCGGGCTGACGTGCATCGTTTCCCTTCTC	120
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Db	293	GCGCTGACAGAAACCGGTTGTCTCTGGCTCTGGGCTGCGCATGCGAGGACGCT	352
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Db	353	GTCCTCATCTACCTCAACCTGGTCCGCGCGCACTTCTCTTCTTACGCGCCACATT	412
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QY	361	TGCGTGTCCATCTGTGGCCATCTGTACACATCGCGCGCGCCGACGATACCTGTCA	420
Db	533	TGCGTGTCCATCTGTGGCCATCTGTGTACACATCGCGCGCGCCGACGATACCTGTCA	592
QY	421	GTCATGTGTCTGCTCTGGGCGCTGTCCCTGCTGCGGAGTATCTCTGGAGTGGATGTC	480
Db	593	GTCATGTGTCTGCTCTGGGCGCTGTCCCTGCTGCGGAGTATCTCTGGAGTGGATGTC	652
QY	481	TGTGACTTCTGTTAGTGGTGTGATCTGTTGGTGTGAACGTCAGATTTCAATACA	540
Db	653	TGTGACTTCTGTTAGTGGTGTGATCTGTTGGTGTGAACGTCAGATTTCAATACA	712
QY	541	ATCGGTGCTGCTGTTTTTTTATGTGTGTTCTCTGTGGGTCCAGCTGTGCTGTGCTG	600
Db	713	ATCGGTGCTGCTGTTTTTTTATGTGTGTTCTCTGTGGGTCCAGCTGTGCTGTGCTG	772
QY	601	AGGATTTCTGTGGATCCCGAAGATGCGGTGTACACGAGGTGTACGTGACCATCTCTC	660
Db	773	AGGATTTCTGTGGATCCCGAAGATGCGGTGTACACGAGGTGTACGTGACCATCTCTC	832
QY	661	ACAGTGTCTGCTTCC-TCCCTGTGGGCTGCGCTTTGGCATTCAGTGGGCGCTGTT	716
Db	833	ACAGTGTCTGCTTCCCTCTGTGGGCTGCGCTTTGGCATTCAGTGGGCGCTT	889

RESULT 2		764 bp mRNA linear EST 21-APR-2001	
BG198766		RST18035 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.	
EST.		BG198766.1 GI:13720453	
KEYWORDS		Homo sapiens (human)	
SOURCE		Homo sapiens	
ORGANISM		Homo sapiens	
REFERENCE		1 (Bases 1 to 764)	
AUTHORS		Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Booser, S., Mays, R., Smith, E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Offenbacher, J., Danzig, J. and Ducar, M.	
TITLE		Creation of genome-wide protein expression libraries using random activation of gene expression	
JOURNAL		Nat. Biotechnol. 19 (5), 440-445 (2001)	
MEDLINE		21227151	
PUBMED		11329013	
COMMENT		Contact: Scott J. Cain	
		Athersys, Inc.	
		3201 Carnegie Ave, Cleveland, OH 44115, USA	
		Tel: 216 431 9900	
		Fax: 216 361 9596	
		Email: scain@athersys.com	
		High quality sequence stop: 559.	
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Query Match		89.6%; Pred. No. 2.3e-131;	
Best Local Similarity		672; Conservative 0; Mismatches 76; Indels 2; Gaps 2;	
Matches		672; Conservative 0; Mismatches 76; Indels 2; Gaps 2;	
QY	187	ATCTACATCTCAACCTGGTGGCGGCGACTTCTCTCTCTAGC-GGCCACATTATG	245
Db	764	ATCTACATCTCAACATGGCGGCGAGCAGACTTCTCTCTCTAGCGCGGCGCTTATATA	705
QY	246	TTGCGCGTTAGCGCTCATCAATAT-CCGCCATCCCATCTCCAAATCTCTAGTCTGTGA	304
Db	704	TTCCCTGTTAGCTTTTCATCAGTATCCCGCCATCAATCTCTAAATCTCTATCTCTGTGA	645
QY	305	TGACCTTTCCCTACTTTATAGCCCTAAGCATGCTGAGCGCCATCAGCACCGAGCGCTGCC	364
Db	644	TGATGTTTCTCTACTTTTCAGGCGCTGAGCTTCTGAGTGCCGTGAGCACCGAGCGCTGCC	585
QY	365	TGTCCATCTCTGTGGCGCATCTGTGTACCACTGCGCGCGCCCGCAGATPACTGTCTAGTCTGA	424
Db	584	TGTCCGCTCTGTGGCGCATCTGTGTACCGCTGCGCACCGCCCGCAGATPACTGTCTAGTCTGA	525
QY	425	TGTGTGCTCTGTGGGCGCTTCTCTGCTGCGGAGTATCTCTGAGTGGATGTTCTGTG	484
Db	524	TGTGTGCTCTGTCTGTGGGCGCTTCTCTGCTGCGGAGCATCTCTGAGTGGATGTTATGTG	465
QY	485	ACTTCTCTGTTAGTGGTCTGATTCTGTTTGGTGTGAAAACGTCAGATTTTCATCAATCG	544
Db	464	GC-TCTCTGTTCAGTGGTGTGATTCTGTGTTGGTGTCAAAACATCAGATTTTCATCAGTCG	405
QY	545	CGTGGCTGTTTTTTTTTATGTGTGTTCTCTGTGGGCTGAGCGCTGTGCTCTGTGTCAGGA	604

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Db      404 CGTGCCTGATTTTTTATGTTGGTTCTCTGTGGTCCAGCCGCTCTGTCATCAGGA 345
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Db      344 TTCTCTGTGGATCCCGAAGATACCAGCTGACGAGCTGTAGTGACCATCTCTCTACAG 285
QY      665 TGCTGGTCTCTCTCTGTGGCTGCCCTTTGGCAATTCAGTGGGCCCTGTTTTCCAGGA 724
Db      284 TACTGGTCTCTCTCTGTGGCTGCCCTTTGGCAATTCAGTGGGCCCTGTTTTCCAGGA 225
QY      725 TCCACTGGATGGAAAGTCTTATTTGTGATGTCATCTAGTTTCCATTTCTCTGTCCG 784
Db      224 TCCAGTGGACAGGAAGTCTTATTTGTGATGTCATCTAGTTTCTATTTCTCTGTCCG 165
QY      785 CTCTTAAACAGCAGTGCACACCCATCATTTACTCTCTGGTGGCTCTTTAGGAGCGTC 844
Db      164 CTCTTAAACAGCAGTGCACACCCATCATTTACTCTCTGGTGGCTCTTTAGGAGCGTC 105
QY      845 AAAATAGGAGAACCTGAACTGCTTCTCCAGAGGCTCTGACGACACGCTGAGGTGG 904
Db      104 AAAATAGGAGAACCTGAACTGCTTCTCCAGAGGCTCTGACGACACGCTGAGGTGG 45
QY      905 ATGAGGTGGAGGGTGGCTTCTCTCAGGAAA 934
Db      44 ATGAGGTGGAGGGAGAAATCTGAGGAAA 15

RESULT 3
BE439409
LOCUS   HTM1-025F1 HTM1 Homo sapiens cDNA, mRNA linear EST 25-JUL-2000
DEFINITION
ACCESSION BE439409
VERSION   BE439409.1 GI:9438891
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Gonzalez,P., Epstein,D.L. and Borras,T.
TITLE    Characterization of gene expression in human trabecular meshwork
          using single-pass sequencing of 1060 clones
JOURNAL  Invest. Ophthalmol. Vis. Sci. (2000) In press
COMMENT  Contact: Pedro Gonzalez
          Department of Ophthalmology
          Duke University
          Duke Eye Center, Erwin Rd, Box 3802, Durham, NC 27710-3802, USA
          Tel: 919 681 4085
          Fax: 919 684 8983
          Email: pedro.gonzalez@duke.edu.
FEATURES
source   1..688
          /organism="Homo sapiens"
          /mol_type="mRNA"
          /db_xref="taxon:9606"
          /tissue_type="Trabecular meshwork"
          /clone_lib="HTM1"

ORIGIN
Query Match 57.8%; Score 559.8; DB 10; Length 688;
Best Local Similarity 98.7%; Pred. No. 6.9e-121;
Matches 627; Conservative 0; Mismatches 2; Indels 6; Gaps 6;

QY      1 ATGGATTCAACCATCCAGTCTTGGGTACAGAACTGACACCAATCAACGACGTGAGGAG 60
Db      60 ATGGATTCAACCATCCAGTCTTGGGTACAGAACTGACACCAATCAACGACGTGAGGAG 119
QY      61 ACTCCTTGCTACAGCAGACCTGAGCTTCAACGGGCTGAGTGCATGCTTTCCCTTGTC 120
Db      120 ACTCCTTGCTACAGCAGACCTGAGCTTCAACGGGCTGAGTGCATGCTTTCCCTTGTC 179
QY      121 GCCTGTACAGGAAACGGGGTGTGCTCTGGCTCTCTGGCTGCGCATGCGCAGGAACGCT 180

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Db      180 GCCTGTACAGGAAACGGGGTGTGCTCTGGCTCTCTGGCTGCGCATGCGCAGGAACGCT 239
QY      181 GTCTTCATCTACATCTCAACCTGGTCGGGCGGACTTCTCTTCTTAGCGGCCACATT 240
Db      240 GTCTTCATCTACATCTCAACCTGGTCGGGCGGACTTCTCTTCTTAGCGGCCACATT 299
QY      241 ATATGTTGCGCGTTAGCGCTCATCAATATCCGCCATCTCCCATCTCCAAAATCTCTCAGTCT 300
Db      300 ATATGTTGCGCGTTAGCGCTCATCAATATCCGCCATCTCCCATCTCCAAAATCTCTCAGTCT 359
QY      301 GTATGACCTTTCCCTACTTATAGGCTTAAGCATGCTGAGCGCCATCAGCACCGAGCGC 360
Db      360 GTATGACCTTTCCCTACTTATAGGCTTAAGCATGCTGAGCGCCATCAGCACCGAGCGC 419
QY      361 TGCTGTGCATCTGTGGCCCATCTGTGTACCACTGCGCGGCCGCCAGATACCTGTCTATCG 420
Db      420 TGCTGTGCATCTGTGGCCCATCTGTGTACCACTGCGCGGCCGCCAGATACCTGTCTATCG 479
QY      421 GTATGTGTGCTGTCTGGGCCCTGTCTCTGCTGGAGTATCTCTGGAGTGGATGTTTC 480
Db      480 GTATGTGTGCTGTCTGGGCCCTGTCTCTGCTGGAGTATCTCTGGAGTGGATGTTTC 539
QY      481 TGTGACTTCTCTGTTTAGTGTCTGATTCTGTTTGTGTGAAACGTCAGATTTTCATTACA 540
Db      540 TGTGACTTCTCTGTTTAGTGTCTGATTCTGTTTGTGTGAAACGTCAGATTTTCATTACA 598
QY      541 ATCGCGTGGCTGTTTTTATGTGTGTTCTCTGTGGTCCAGCTGCTGCTGCTGCTGCTC 600
Db      599 ATCGCGTGGCTGTTTATGTGTGTTCTCTGTGGTCCAG-CTGGTCTCTGCTGCTGCTC 655
QY      601 AGGATTCCTGTGTGATCCCGGAAGATGCCGCTGAC 635
Db      656 AGGA-TCTCTGTGAT-CCGGAAGATGCAGCTGAC 688

RESULT 4
BG208126/c
LOCUS   BG208126 787 bp mRNA linear EST 21-APR-2001
DEFINITION
ACCESSION RST27616 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
VERSION   BG208126
KEYWORDS BG208126.1 GI:13729813
SOURCE   EST.
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
          Cain,S., Leventhal,C., Thornton,M., Ramachandran,R.,
          Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Booser,S.,
          Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K.,
          Offenbacher,J., Danzig,J. and Ducar,M.
          Creation of genome-wide protein expression libraries using random
          activation of gene expression
JOURNAL  Nat. Biotechnol. 19 (5), 440-445 (2001)
MEDLINE  21227151
PUBMED   11329013
COMMENT  Contact: Scott J. Cain
          Athersys, Inc.
          3201 Carnegie Ave, Cleveland, OH 44115, USA
          Tel: 216 431 9900
          Fax: 216 361 9596
          Email: scain@athersys.com
          High quality sequence stop: 553.
          Location/Qualifiers
FEATURES
source   1..787
          /organism="Homo sapiens"
          /mol_type="mRNA"
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          /cell_line="HT1080"
          /clone_lib="Athersys RAGE Library"
          /note="See 'Creation of Genome-wide Protein Expression

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Db 101 TAGCAGCGTCAAAATAGCGAAGACCTGAAGCTGTTCTCCAGAGGCTCTGCAGGAGCG 42
QY 894 GCCTGAGGTGATGAAGGTGAGGGTGGCTTCCTCAGGAAA 934
Db 41 GTCTGAGGTGATGAAGGTGAGGGCAGCTACCTGAGGAAA 1

RESULT 6
CD051096 924 bp mRNA linear EST 09-MAY-2003
DEFINITION AGENCOURT_13981113 NIH_MGC_173 Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CD051096
VERSION CD051096.1 GI:30488660
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 924)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cchapbs-remail.nih.gov
Tissue Procurement: Dr. Jamie Thompson, University of WI
CDNA Library Preparation: Gina Zastrow-Hayes
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDRM39 row: e column: 24
High quality sequence start: 3
High quality sequence stop: 741.
FEATURES
source
1. 924
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/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic trophoblasts, made from WA01 stem
cells"
/lab_host="DH10B TonA"
/clone_lib="NIH MGC 173"
/notes="Vector: pDONR201; Site 1: attP2; Site 2: attP1;
LIBR PRIMING - oligo dr; METHOD - full-length enriched;
LIBR PROVIDER - Bradfield"

ORIGIN
Query Match 47.2%; Score 457.2; DB 14; Length 924;
Best Local Similarity 88.0%; Pred. No. 1.1e-96;
Matches 521; Conservative 0; Mismatches 68; Indels 3; Gaps 2;

QY 1 ATGGATTCAACATCCCAAGTCTTGGGTACAGAACTGACCAATCAACGACGTGAGGAG 60
Db 269 ATGGATCAACATCTCAACTTGGACACAGAACTGACCAATCAACGAACTGAGGAG 328
QY 61 ACTCCTTCCTCAACGACAGCCTGAGTTCACGGGGTACGTCATCGTTTCCCTTGTGTC 120
Db 329 ACTCTTCTCAACGACAGCTTGAAGCTTCAGGCTTCAGTGTGATCGTTTCCCTTGTGTC 389
QY 121 GCGCTGACAGGAAACGCGGTGTGTGCTGTGGCTTCGCGCTCCGCATGCGCAGGAACGCT 180
Db 389 GGGCTGACAGGAAACGCGGTGTGTGCTGTGGCTTCGCGCTCCGCATGCGCAGGAACGCGC 448
QY 181 GTCTCCATCTACATCTCAACTGCTGCGGGCGCACTTCCTTCCTTAGCGGCACATT 240
Db 449 TTCTCCATCTACATCTCAACTGCTGCGGGCGCACTTCCTTCCTTAGCGGCAGCTT 508
QY 241 ATATGTTCCGCGGTACGCGCTCATCAATATCGGCCATCCATCTCCAAAATCCTCAGTCCCT 300
Db 509 ATATATTCCTCTTAAGCTTTCATCAGTATCCCCCATACCACTCTAAAATCCTCTATCCT 568
QY 301 GTGATGACCTTTCCTACTTTATAGGCTTAAGCATGTGTGAGGGCGCATCAGCAGCGGCG 360
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Db 569 GTGATGATGTTTCTTCTACTTTTCAGGCGCTGAGCTTTCGAGTGCCTGAGCACCGAGCGC 628
QY 361 TGCCCTGTCCATCCTGTGGCCCATCTGTGTACCACTGCCCGCCGACAGATACCTGTGTCATC- 419
Db 629 TGCCCTGTCCGCTCCTGTGGCCCATCTGTGTACCGCTGCCACCGCCACACACCTGTGACGN 688
QY 420 GGTTCATGTGTGCTGCTGCTGGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 479
Db 689 GGTGATGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 748
QY 480 CTGTGACATCTCCCTGTTTGTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 539
Db 749 ATGTGCTTCCCTGTTTCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 808
QY 540 AATCGCGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 589
Db 809 AGTCGCGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 860

RESULT 7
AQ888076 503 bp DNA linear GSS 10-NOV-1999
LOCUS HS_2142_B2_F08_T7C CIT Approved Human Genomic Sperm Library D Homo
DEFINITION sapiens Genomic clone Plate=2142 Col=16 Row=L, genomic survey
sequence.
ACCESSION AQ888076
VERSION AQ888076.1 GI:6344266
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 503)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
10449764
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 2142 Row: L Column: 16
Seq primer: T7
Class: BAC ends
High quality sequence stop: 503.
FEATURES
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1. 503
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E-Coli DH10B"

ORIGIN
Query Match 37.0%; Score 358.8; DB 28; Length 503;
Best Local Similarity 87.3%; Pred. No. 1.3e-73;
Matches 393; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 255 AGCCCTCATCATATCCGCCATCCCATCTCCAAAATCCTCAGTCTGTGATGACCTTCC 314
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Db 52 AAGCTTCATCAGTATCCGCCATCACCATCTCTAAATCCTCTATCTATCTGCGATGATTTTC 111
 QY 315 CTACTTTATAGGCTAAGCATGCTGAGCCATCAGCACCGAGCGCTGCTGCTCCATCCT 374
 Db 112 CTACTTTGAGGCTGAGCTTCTGAGTGGCTGAGCAGCGCTGCTGCTGCTGCT 171
 QY 375 GTGCGCCATCTGTATACATGCGCGCGCCAGATACCTGTATCGTATGATGCTTCC 434
 Db 172 GTGCGCCATCTGTATACATGCGCGCGCCAGATACCTGTATCGTATGATGCTTCC 231
 QY 435 GCTCTGGCGCTGCTGCTGCGGAGTATCTGAGTGGATGTTCTGATCTTCCGTT 494
 Db 232 GCTCTGGCGCTGCTGCTGCGGAGTATCTGAGTGGATGTTCTGATGCTTCCGTT 291
 QY 495 TAGTGTGTGATCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 554
 Db 292 CAGAGTGTGATCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 351
 QY 555 TTTTATATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 614
 Db 352 TTTTATATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 411
 QY 615 ATCCGGAAGATCCGCTGACAGGCTGTACGTGACCATCTCTCAGTGTGTTT 674
 Db 412 ATCCGGAAGATCCGCTGACAGGCTGTACGTGACCATCTCTCAGTGTGTTT 471
 QY 675 CTTCTCTGTGGCTGCGCTTTGGCATTCA 704
 Db 472 CTTCTCTGTGGCTGCGCTTTGGCATTCA 501

RESULT 8

B74348
 LOCUS CIT-HSP-2042L7.TF CIT-HSP Homo sapiens genomic clone 2042L7,
 genomic survey sequence.

ACCESSION B74348.1 GI:2770035

VERSION GSS.

KEYWORDS Homo sapiens (human)

SOURCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

ORGANISM Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 468)

AUTHORS Adams,M.D., Rounsley S.D., Field,C.E., Bass,S., Linher,K.,

Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H.,

Simon,M., and Venter,J.C.

TITLE Use of a random BAC End Sequence Database for Sequence-Ready Map

JOURNAL Building

COMMENT Unpublished (1997)

Other GSSs: CIT-HSP-2042L7.TR

Contact: Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

TEL: 301 838 0200

Fax: 301 838 0208

Email: mdadams@tigr.org

Clones are available from Research Genetics (info@resgen.com). BAC

end search page:

http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html

Seq primer: M13-21

Class: BAC ends.

Location/Qualifiers

1. 468

/organism="Homo sapiens"

/mol_type="genomic DNA"

ORIGIN
 Query Match 35.8%; Score 347; DB 28; Length 468;
 Best Local Similarity 90.3%; Pred. No. 7.3e-71;
 Matches 371; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 255 AGCGCTCATCAATATCCGCCATCCCATCTCCAAATCCTCAGTCTCTGTATGATGATTTTC 314
 Db 57 AAGCTTCATCAGTATCCGCCATCACCATCTCTAAATCCTCTATCTGATGATGATTTTC 116
 QY 315 CTACTTTATAGGCTAAGCATGCTGAGCCATCAGCACCGAGCGCTGCTGCTCCATCCT 374
 Db 117 CTACTTTGAGGCTGAGCTTCTGAGTGGCTGAGCAGCGCTGCTGCTGCTGCT 176
 QY 375 GTGCGCCATCTGTATACATGCGCGCGCCAGATACCTGTATCGTATGATGCTTCC 434
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 Db 232 GCTCTGGCGCTGCTGCTGCGGAGTATCTGAGTGGATGTTCTGATGCTTCCGTT 296
 QY 495 TAGTGTGTGATCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 554
 Db 292 CAGTGTGTGATCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 356
 QY 555 TTTTATATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 614
 Db 352 TTTTATATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 416
 QY 615 ATCCGGAAGATCCGCTGACAGGCTGTACGTGACCATCTCTCAGTGTGTTT 665
 Db 412 ATCCGGAAGATCCGCTGACAGGCTGTACGTGACCATCTCTCAGTGTGTTT 467

RESULT 9

AK029369

LOCUS

DEFINITION

AK029369

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

AK029369 2075 bp mRNA linear HTC 18-SEP-2003
 Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched
 library, clone:483406120 product:MrpB2 G protein-coupled receptor,
 full insert sequence.

ACCESSION AK029369.1 GI:26325335

VERSION HTC; CAP trapper

KEYWORDS Mus musculus (house mouse)

SOURCE Mus musculus

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE 1

Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

REFERENCE 2

Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,

Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20493374

PUBMED 11042159

REFERENCE 3

Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,

Konno,H., Akiyama,J., Nishi,K., Kitsuai,T., Tashiro,H., Itoh,M.,

Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,

Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,

/note="Vector: pBelOBAC11; Site_1: HindIII; Site_2:
 HindIII"

QY 255 AGCGCTCATCAATATCCGCCATCCCATCTCCAAATCCTCAGTCTCTGTATGATGATTTTC 314
 Db 57 AAGCTTCATCAGTATCCGCCATCACCATCTCTAAATCCTCTATCTGATGATGATTTTC 116
 QY 315 CTACTTTATAGGCTAAGCATGCTGAGCCATCAGCACCGAGCGCTGCTGCTCCATCCT 374
 Db 117 CTACTTTGAGGCTGAGCTTCTGAGTGGCTGAGCAGCGCTGCTGCTGCTGCT 176
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 QY 435 GCTCTGGCGCTGCTGCTGCGGAGTATCTGAGTGGATGTTCTGATCTTCCGTT 494
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 Db 292 CAGTGTGTGATCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 356
 QY 555 TTTTATATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 614
 Db 352 TTTTATATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 416
 QY 615 ATCCGGAAGATCCGCTGACAGGCTGTACGTGACCATCTCTCAGTGTGTTT 665
 Db 412 ATCCGGAAGATCCGCTGACAGGCTGTACGTGACCATCTCTCAGTGTGTTT 467

AK029369 2075 bp mRNA linear HTC 18-SEP-2003
 Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched
 library, clone:483406120 product:MrpB2 G protein-coupled receptor,
 full insert sequence.

ACCESSION AK029369.1 GI:26325335

VERSION HTC; CAP trapper

KEYWORDS Mus musculus (house mouse)

SOURCE Mus musculus

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE 1

Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

REFERENCE 2

Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,

Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20493374

PUBMED 11042159

REFERENCE 3

Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,

Konno,H., Akiyama,J., Nishi,K., Kitsuai,T., Tashiro,H., Itoh,M.,

Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,

Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,

/note="Vector: pBelOBAC11; Site_1: HindIII; Site_2:
 HindIII"

QY 255 AGCGCTCATCAATATCCGCCATCCCATCTCCAAATCCTCAGTCTCTGTATGATGATTTTC 314
 Db 57 AAGCTTCATCAGTATCCGCCATCACCATCTCTAAATCCTCTATCTGATGATGATTTTC 116
 QY 315 CTACTTTATAGGCTAAGCATGCTGAGCCATCAGCACCGAGCGCTGCTGCTCCATCCT 374
 Db 117 CTACTTTGAGGCTGAGCTTCTGAGTGGCTGAGCAGCGCTGCTGCTGCTGCT 176
 QY 375 GTGCGCCATCTGTATACATGCGCGCGCCAGATACCTGTATCGTATGATGCTTCC 434
 Db 172 GTGCGCCATCTGTATACATGCGCGCGCCAGATACCTGTATCGTATGATGCTTCC 236
 QY 435 GCTCTGGCGCTGCTGCTGCGGAGTATCTGAGTGGATGTTCTGATCTTCCGTT 494
 Db 232 GCTCTGGCGCTGCTGCTGCGGAGTATCTGAGTGGATGTTCTGATGCTTCCGTT 296
 QY 495 TAGTGTGTGATCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 554
 Db 292 CAGTGTGTGATCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 356
 QY 555 TTTTATATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 614
 Db 352 TTTTATATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 416
 QY 615 ATCCGGAAGATCCGCTGACAGGCTGTACGTGACCATCTCTCAGTGTGTTT 665
 Db 412 ATCCGGAAGATCCGCTGACAGGCTGTACGTGACCATCTCTCAGTGTGTTT 467

AK029369 2075 bp mRNA linear HTC 18-SEP-2003
 Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched
 library, clone:483406120 product:MrpB2 G protein-coupled receptor,
 full insert sequence.

ACCESSION AK029369.1 GI:26325335

VERSION HTC; CAP trapper

KEYWORDS Mus musculus (house mouse)

SOURCE Mus musculus

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE 1

Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

REFERENCE 2

Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,

Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20493374

PUBMED 11042159

REFERENCE 3

Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,

Konno,H., Akiyama,J., Nishi,K., Kitsuai,T., Tashiro,H., Itoh,M.,

Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,

Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,


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AQ696198      620 bp      DNA      linear      GSS 06-JUL-1999
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DEFINITION
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  sapiens genomic clone Plate=2142 Col=7 Row=L, genomic survey
  sequence
ACCESSION
AQ696198
VERSION
AQ696198.1 GI:5386446
KEYWORDS
GSS.
SOURCE
Homo sapiens (human)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 620)
  Mahairas G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., and
  Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D., and
  Hood, L.
  Sequence-tagged connectors: A sequence approach to mapping and
  scanning the human genome
  Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
  99380589
  10449764
  Contact: Mahairas GG, Wallace JC, Hood L
  High Throughput Sequencing Center
  University of Washington
  401 Queen Anne Avenue North, Seattle, WA 98109, USA
  Tel: (206) 616-3618
  Fax: (206) 616-3887
  Email: jwallace@u.washington.edu
  Clones may be purchased from Research Genetics (info@resgen.com).
  BAC end Web Server: http://www.htsc.washington.edu
  Plate: 2142 row: L column: 7
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  Class: BAC ends
  High quality sequence stop: 620.
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Matches 388; Conservative 0; Mismatches 53; Indels 2; Gaps 2;
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DB 53 AAGTTTCATCATGATTC -CCATACCATCTCTATATCTCTATCTCTGTGATGATGTTTC 111
QY 315 CTATTTATAGGCTAAGCATGTGAGCGCCATCAGCACCGAGCGCTGCTGTCCATCCT 374
DB 112 CTACTCTGCAAGCTGAGCTTCTGAGTGCCTGAGCAGCAGCGCTGCTGCTGCTCT 171
QY 375 GTGCCCATCTGTGTACCACTGCGCGCCGCCATACCTGCTATCGGTGATGTGCTCT 434
DB 172 GTGCCCATCTGTGTACCGCTGCGCACCGCCCCACACACCTGTAGCGGTGGTGTGCTCT 231
QY 435 GCTCTGGGCCCTGTCCCTGTGTCGGAGTATCTCTGGAGTGGATGTTCTGTGACTTCTCTTT 494
DB 232 GCTCTGGGCCCTGTCCCTGTGTCGGAGATCTCTGGAGTGGATGTTATGTGGCTTCTCTGT 291
QY 495 TAGTGGTGTGCTGATTTCTTTGGTGTGAACGTCAGATTTTCATTACATCGGTGGCTGTGT 554
DB 292 CAGTGGTGTGATTTCTCTTTGGTGTCAACATCATATTTTCATCATGTCGGGTGGCT-GA 350
QY 555 TTTTATATGTGTGTTCTCTGTGGTCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 614

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Db 351 TTTTATATGTGTGTTCTCTGTGGTCCAGCTGCTCTGCTGATCAGGATTTCTGTGG 410
QY 615 ATCCCGGAGATGCGCTGACAGGCTGTAGTGACCATCTCTCTACAGTGTGTGTTCT 674
DB 411 ATCCCGGAGATACCGCTGACAGGCTGTAGTGACCATCTCTCTACAGTGTGTGTTCT 470
QY 675 CTTCTCTGTGGCTGCGCTTGTG 697
DB 471 TCTCTCTGTGGCTGCGCTTGTG 493

CD243595      905 bp      mRNA      linear      EST 22-MAY-2003
LOCUS
DEFINITION
  AGENCOURT 14121139 NIH MGC_180 Homo sapiens cDNA clone
  IMAGE:30393708 5', mRNA sequence.
CD243595
VERSION
CD243595.1 GI:31004059
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 905)
  NIH-MGC http://mgi.nci.nih.gov/
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished (1999)
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-remail.nih.gov
  cDNA Library Preparation: Invitrogen Corp
  cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
  DNA Sequencing by: Agencourt Bioscience Corporation
  Clone distribution: MGC clone distribution information can be
  found through the I.M.A.G.E. Consortium/LLNL at:
  http://image.llnl.gov
  Plate: NDAM447 row: P column: 21
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  High quality sequence stop: 592.
  Location/Qualifiers
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      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /clones="IMAGE:30383708"
      /lab_host="DH10B-Ton A ( T1 and T5 phage resistances)"
      /note="Organ: Testis; Vector: pCMV-SPORT6.1; Site 1: NotI;
        Site 2: EcoRV (destroyed); Library is oligo-dT primed and
        directionally cloned (Scorv site is destroyed upon
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        constructed by (Invitrogen). Note: this is a NIH_MGC
        Library."
ORIGIN
Query Match      30.7%; Score 297.4; DB 14; Length 905;
Best Local Similarity 95.9%; Pred. No. 4.7e-59;
Matches 327; Conservative 0; Mismatches 11; Indels 3; Gaps 2;
QY 1 ATGATTCAACATCCAGTCTTGGTACAGACTGACCAATCAACGAGCTGAGGAG 60
DB 390 ATGATTCAACATCCAGTCTTGGTACAGACTGACCAATCAACGAGCTGAGGAG 449
QY 61 ACTCTTCTCTAACAAGACACCTGAGTTTACGGGGCTGACGTGCAATCGCTTCCCTTGTTC 120
DB 450 ACTCTTCTCTAACAAGACACCTGAGTTTACGGGGCTGACGTGCAATCGCTTCCCTTGTTC 509
QY 121 GCGCTGACAGAAACCGGTTGTCTCTGCTCTCTGGCTGCGCATGCGCAGAACGCT 180
DB 510 GCGCTGACAGAAACCGGTTGTCTCTGCTCTCTGGCTGCGCATGCGCAGAACGCT 569
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Db      570 GTCTCCATCTACATCCTCAACCTGTCGCGCGCGACTTCCTCTCTCTTAGCGGCGACATT 629
Qy      241 ATATGTTCCGCGTTACGCTCATCAATAT-CCGCCATCCCATCTCCAAAATCCTCAGTCC 299
Db      630 ATACGTTCCGCGTTACGCTCATCAATATCCGCCATCCCTTCCAAAATCCTCAGTCC 689
Qy      300 TGTG--ATGACCTTTCCCTACTTTATAGGCTTAAGCATGCT 338
Db      690 TGTGATGACCTTTTCCCTACTTTATAGGCTTAAGCATGCT 730

RESULT 12
LOCUS   BI828553
DEFINITION 618 bp mRNA linear EST 04-OCT-2001
        60307843F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5170163 5',
        mRNA sequence.
ACCESSION BI828553
VERSION   BI828553.1 GI:15940103
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: c9apbs@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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    anonymous male age 27. Library is oligo-dT primed and
    directionally cloned (EcoRV site is destroyed upon
    cloning). Average insert size 1.3 kb, insert size range
    0.9-3 kb. Library is normalized and enriched for
    full-length clones and was constructed by C. Gruber
    (Invitrogen). Research Genetics tracking code 013. Note:
    this is a NIH_MGC Library."
ORIGIN
Query Match 29.5%; Score 285.6; DB 12; Length 618;
Best Local Similarity 74.5%; Pred. No. 2.4e-56;
Matches 395; Conservative 0; Mismatches 114; Indels 21; Gaps 2;

Qy      1 ATGGATTCAACCATCCAGCTTTGGTACAGACTGACACCAATCAACGGACGTGAGGAG 60
Db      89 ATGGATCCAAACCCCGGCTTGGGGAACAGAAATACAAAGTGAATGGAAATGACCAA 148
Qy      61 ACTCCT-----TGCTACAAGCAGACCTTCAGCTTTCACGGGCTGACGTGCATCGTT 111
Db      149 GCGCTTCTTCTGTTTGTGGCAAGAGACCCCTGATCCCGGTCTTCTGTATCCTTTTCATT 208
Qy      112 TCCTTGTGCGCTGACGAAACCGGTTTGCTCTGCTCTGCTGGCTGGCGATGCGC 171
Db      209 GCGCTGTGCTGGCTGGTAGAAACCGGTTTGTGCTCTGCTCTGCTGGCTTCGGCATGCGC 268

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Qy      172 AGGAACGCTGTCTCCATCTACATCCTCAACCTGTCGCGCGCGACTTCCTCTTCTTAGC 231
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Qy      232 GGCCACATATATGTTGGCGGTACCGCTCATCAATATCGGCATCCCATCCCAAAA-- 289
Db      329 TTCCAGATTATAAATTGCCCTGGGTACCTCAGTAACCTTCTTGTTCCATCTCCATCAAT 388
Qy      290 -----TCCTCAGTCTCTGTGATGACCTTTCCCTACTTTATAGGCTTAAGCATGCTG 339
Db      389 TTCCCTAGCTTCTTCCACCATGTGATGACCTGTGCCTACTTTCAGGCGCTGAGCATGCTG 448
Qy      340 AGCGCCATCAGCACCGAGCGCTCCCTGTCATCTCTGTCGCCCATCTGGCCCATCTGGTACCACTGCCGC 399
Db      449 AGCACCGTTCAGCACCGAGCGCTCCCTGTCGCTCTGTCGCCCATCTGGTATCGCTCCGC 508
Qy      400 CGCCCCCAGATACCTGTCTCATCGGTCACTGTGTCTCTCTCTGCGCCCTGCTCCCTGTCGCG 459
Db      509 CGCCCCCAGACACCTGTTCAGCGGTCTGTGTCTCTCTCTGCGCCCTGCTCCCTACTGCTG 568
Qy      460 AGTATCCTGGAGTGGATGTTCTGTGACTCTCTCTCTCTCTGTTAGTGGTGTCTGATTC 509
Db      569 AGCATCTTGGAGGGAAGTTCTGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 618

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RESULT 13

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LOCUS   BY741352
DEFINITION 704 bp mRNA linear EST 31-DEC-2002
        CDNA clone G370060H08 5', mRNA sequence.
ACCESSION BY741352
VERSION   BY741352.1 GI:27166203
KEYWORDS  EST.
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 704)

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AUTHORS  Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
        Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
        Kiyosawa,H., Vagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
        Schonbach,C., Cojocari,T., Baldarelli,R., Hill,B.P., Bult,C.,
        Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
        Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
        Chothia,C., Cousins,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
        Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
        Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
        Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
        Kawaji,H., Kawasawa,Y., Kedierski,R.M., King,B.L., Konagaya,A.,
        Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
        Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
        Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
        Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
        Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
        Saitanin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,
        Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomika,M.,
        Valverde,R., Wagner,L., Wahlstedt,C., Wang,Y., Watanabe,Y.,
        Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
        Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
        Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
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        Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Inotani,K., Ishii,Y.,
        Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sakaki,D., Shibata,K.,
        Shingawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
        Rogers,J., Birney,E. and Hayashizaki,Y.
        Analysis of the mouse transcriptome based on functional annotation
        of 60,770 full-length cDNAs
        Nature 420, 563-573 (2002)

```

TITLE

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JOURNAL  Nature
MEDLINE  22354683
FUBMED   12468951

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COMMENT  Contact: Yoshihide Hayashizaki
        Laboratory for Genome Exploration Research Group, RIKEN Genomic

```

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Tel: 81-45-503-9222
Fax: 81-45-503-9216

Email: genome-res@sc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P.,
Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, P.,
Inotani, K., Ishii, F., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y.,
Kondo, S., Konno, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M.,
Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Saito, R., Sakazume, N.,
Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M.,
Takeda, Y., Waki, K., Watahiki, A., Muramatsu, M., and Hayashizaki, Y.
Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.

Cells were provided by Drs. William J Pavan, Stacie Loftus, and
Denise Larson (Division of Intramural Research Genetic Disease
Research Branch National Human Genome Research Institute, National
Institutes of Health (NIH) Building: 49, Room 4A82 49 Convent Drive
MSC 4472 Bethesda, Maryland U.S.A) whose assistance we gratefully
acknowledge.

Please visit our web site (<http://genome.gsc.riken.go.jp>) for
further details.

FEATURES source

Location/Qualifiers
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/clone="G37060H08"
/cell_type="B16 F10Y cells"
/clone_lib="RIKEN full-length enriched, B16 F10Y cells"

ORIGIN

Query Match 29.4%; Score 284.6; DB 13; Length 704;
Best Local Similarity 65.0%; Pred. No. 4.3e-56;
Matches 435; Conservative 0; Mismatches 231; Indels 3; Gaps 1;
QY 253 TTACGCTCATCAATACCGCCATCCCATCTCCAAAATCCATAGTCCTGTGATGACCTTT 312
DB 23 TTACACATCTACTTCATCCCACTAATTTTTCATCTTACATAGTGTGTTAAACATT 82
QY 313 CCCTACTTTAGCCCTAAGCATCTGCGCCATCAGCCAGCCGCTGCCCTGTCATC 372
DB 83 GTTACCTTTAGTCTGAGCATCTTCACTGTCTATTAGCACTGAACCTTCCCTATCTGTC 142
QY 373 CTGTGGCCCATCTGTTACCACTGCGCGCCGCCACAGATACCTGTTCATCGTGTGTGTC 432
DB 143 ATGTGGCCCATCTGTTACCGCTGCCAAGCCCAAGGCACACATCAGCTGTCTATGTACT 202
QY 433 CTGCTCTGGGCGCTGCTCTCGGAGTATCTGGAGTGGATGTTCTGTGACTTCCTG 492
DB 203 GTGCTTTGGGCTCTTGTCCCTGGTGTGAGCCCTCTCTGGAAGAAAGGAATGTGGCTTCCCTA 262
QY 493 TTTAGTGTGTGATCTCTGTTTGTGTGAACAGTCAGATTTCAATTACAATCGGCTGTGCTG 552
DB 263 TATTACACTAGTGGCCCTGTTTGTGTGAAGACATTTGATTTAATCACTACTGATGATGTTA 322

QY 553 GTTTTTTATGTGTGTTCTCTGTGGTCCAGCTGTGCTGTGGTCAGGATTTCTCTGT 612
DB 323 ATTGTTTTTATTTGGTTCCTCTTGGATCCAGCTGTGCCCTTGTGCTTACCACTTCTGT 382
QY 613 GGATCCCGGAAGATGCGCTGACACAGCTGTAGCTGACCATCCCTCTCACAGTGTCTGTGTC 672
DB 383 GGCTTACACAAGGTTCTCTGTGACCAAGTTGTATGTGACCATTTGTGTTTACAGTGTCTGTGTC 442
QY 673 TTCTCTCTGTGTGCTGCTGCTTGGCAATTCAGTGGGCGCTGTTTCCAGGATCCACCTG 732
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DB 503 TTTCATGATATAAACCTTTGTGGTTTTCGTAACGTGACAATATTTCTGCTGTGATTAAC 562
QY 793 AGCAGTGCACACCCCATCATTTACTTCTTGTGGCTCTTGTAGGAGCTC---AAAAT 849
DB 563 AGCTGTGCCAACCCCATCATTTACTTCTTGTGGCTCTTGTAGGACCATCGGTTTCAA 622
QY 850 AGGCAGAACCTTGAAGCTGTTCTCCAGAGGCTCTGCAGGACACGCTGAGGTGGATGAA 909
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QY 910 GGTGAGGG 918
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RESULT 14

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LOCUS Leukos2_3_G11_91_A024 Stimulated peripheral blood leukocytes S2
DEFINITION Equus caballus cDNA clone Leukos2_3_G11_A024 5', mRNA sequence.
ACCESSION CD469424
VERSION CD469424.1 GI:31390692
KEYWORDS EST.
SOURCE Equus caballus (horse)
ORGANISM Equus caballus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
1 (bases 1 to 783)
AUTHORS Vandenplas, M., Cordonnier-Pratt M.-M., Suzuki, Y., Sugano, S.,
Moore, J. N., Liang, C., Sun, F., Sullivan, R., Shah, M., and Pratt, L. H.
TITLE An EST database from equine (Equus caballus) stimulated peripheral
blood leukocytes
JOURNAL Unpublished (2003)
COMMENT Other ESTs: Leukos2_3_G11.b1_A024
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
the Human Genome Center, University of Tokyo Institute of Medical
Science; tissue and RNA were prepared in the Department of Large
Animal Medicine, University of Georgia; sequencing done in the
Laboratory for Genomics and Bioinformatics, University of Georgia.
Sequence ends have been trimmed to exclude vector and regions below
Phred quality 16. Three-prime sequences are presented as their
reverse complement and have been trimmed to exclude polyA.
Seq primer: Sug5 (CTTCGCTCTCTAAAGTCGCG).

FEATURES source

Location/Qualifiers
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/strain="thoroughbred"
/db_xref="taxon:9796"
/clone="Leukos2_3_G11_A024"
/sex="male"

